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Sequence 2755, A Sequence 11893, A Sequence 12776, A Sequence 12940, A Sequence 22, Appl Sequence 2813, Appl Sequence 14222, A Sequence 4346, Appl Sequence 9, Appli
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

(cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Sequence 22, Appl Sequence 12378, A Sequence 12378, A Sequence 12378, A Sequence 16284, A Sequence 16284, A Sequence 16243, A Sequence 11394, A Sequence 11310, A Sequence 11310, A Sequence 1134, A Sequence 1134, A Sequence 54021, A Sequence 54021, A Sequence 54021, A Sequence 54021, A Sequence 108654, Sequence 108654, Sequence 108654, A Sequence 108654,		attggatgttggccatcgaggtgcaggaaactctacaacaactgcccagctggctaaagt 	tcaagaaatactattgcttctttaagaaatgctgctagtcatggtggtgcctttgtaga 	ATTIGACGIACACCTITCAAAGGACTITGIGCCCGIGGIAIAICATGAICTIACCIGITG	TTGACTATGAAAAAGAAATTTGATGCTGATCCAGTTGAATTATTTGAAATTCCAGTAAA 	agaattaacatttgaccaactccagttgttaaagctcactca
Sequence Seq	SCTTCCTATGCGCGGTGCAG TTCCAAGTATTGGAAGCCAAGA 	JAACAACTGCCCAGCTGGCT TTACATTGCAGACGCTCCT	AGTCATGGTGCAGCCTTT GAACATCACGCAGACATG	STATATCATGATCTTACC \TTTATCAGGATTTCGGA	AATTATTTGAAATTCCA 	ACTCATGTGACTGCACTG TCTCTGTGATCGCAGGC
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; Sequence 36, Application US/08883795A
; Patent No. 5985607
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APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor
ITILE OF INVENTION: Recombinant
TITLE OF INVENTION: Vectors for
NUMBER OF SEQUENCES: 39
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ZIP: M5H 3Y2
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STATE: Ontario
COUNTRY: Canade
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2.1%; Score 68.4; DB 4; Length 27
Best Local Similarity 44.7%; Pred. No. 1.9e-07;
Matches 409; Conservative 0; Mismatches 491; Indels
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Sequence 11893, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TILLE OF INVENTION: Nucleic acids and proteins of FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 11893
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                                                                 1655 griggangrecarrigacrecreargerericrecrearinarcacarringere
                                                                                                                                                                                                                                                                     1398 TAAGGATCGGAAAGAATCTGTGGTTCAGGAGGAAAATTCCTTTTCAGAAAATCAGCCATT
                                                                                                                               1278 ITTGACTATGAAAAAGAAATTTGATGCTGATCCAGTTGAATTATTTGAAATTCCAGTAAA
ATTTGACGTACACCTTTCAAAGGACTTTGTGCCCGTGGTATATCATGATCTTACCTGTTG
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Tissue Plasminogen Activator
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.25
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TYPE: DNA
ORGANISM: Human
FEATURE:
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                                                                                                                                      LENGTH:
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Patent No. 6812339
GERERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION:
MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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Pred. No. 1.9e-05;
0; Mismatches 239; Indels
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              APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
                                                             ATTORNEY/AGENT INPORMATION:
NAME: Gravelle, micheline
REGISTRATION NUMBER: 40.241.
REFRENCE/DOCKET NUMBER: 7841-
TELECOMMUNICATION INFORMATION:
TELEFHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INPORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.9%;
Best Local Similarity 47.1%;
Matches 214; Conservative
                                                                                                                                                                                                                      LENGTH: 665 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens IMMEDIATE SOURCE:
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                               CDNA
                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                CLASSIFICATION:
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US-08-883-795A-36
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Sequence 15940, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
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                  PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREUESC for Windows Version ASC ID NO 12776
                                                                                                                                                                                                                                                                                                      | NAME/KEY: misc_feature
| LOCATION: (1)...(187169)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12776
                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%;
FILING DATE: 2000-10-20
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Matches 257; Conservative
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LENGTH: 1141
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                                                                   TYPE: DNA
                                                                                          FEATURE:
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1.8%; Score 57.8; DB 4; Length 1
Best Local Similarity 43.6%; Pred. No. 0.0012;
Matches 257; Conservative 0; Mismatches 332; Indels
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FBAELSEQ for Windows Version 4.0
SEQ ID NO 15940
LENGTH: 191569
                                                                                                                                     | FEATURE:
| NAME/KEY: misc_feature
| LOCATION: (1)...(191569)
| OTHER INFORMATION: n = A,T,C or G
| US-09-949-016-15940
                                                                                                                              ORGANISM: Human
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Sequence 22, Application US/09806708B
Patent No. 6784342
GENERAL INFORMATION:
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT PILLING DATE: 2001-04-03

RESULT 6 US-09-806-708B-22

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AACTGCACAAATCTTTGTGCCATCTTGTATATAGGTATTTTTTACATGGGTTGACATGCA 2678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 KYHMMNNNGCBTVTWMVRXKTDRDWSBKRNNYGMBWWKNWSYDVTYYWWVWDDMCKRKVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                540 YAAWYTKSSWNYTSRYYRWKTNNSWRWRSDTRSMGRANNYARABHY----GYKWNTRWB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 ABVNSTCTTWKSKTTKVRTSCWANNCRAGDANKDHKWWKWSAAMGVYMNNNNNNNNTYKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1961 TAATTTATGATAGGATATATGATTGGATGCCTGAACAACCAAATATATTCCAAGTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 ARHBARWDWVWHSAWKKWHANAAHYSRKKWTBYRKTRYNNNNGTTWWKRWWAWYWKUDM
                                                                                                                                                                                                                                                                                                                                                                                                                         1841 TCAGAAACCCATCCTATATTCAAGAGGCAAAAGCTAAGGGACTAGTCATATTCTGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                     NAME/KEY: promoter

LOCATION: (1)..(1141)

COMMET INFORMATION: consensus sequence of A.t., L.a., and B.n.
US-09-806-708B-22
                                                                                                                                                                                                                                                                                                                                  Length 1141;
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 11.2%; Pred. No. 0.00011;
Matches 121; Conservative 395; Mismatches 556;
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
                                                                                                                                                                         ORGANISM: Artificial sequence
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Pred. No. 0.00079;

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50.68;
                Matches 159; Conservative
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ORGANISM: Homo sapiens
 Best Local Similarity
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US-09-621-976-2813
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LOCATION: 235
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                                                                                                    2794 TTACATCAATGTTAAAATTTCAAAATGCTGCAGGGTAATTTAATGTATAAAATTTTAGTA 2853
                                                                                                                                                                                                                                  CACAACACCATTTTCATTCAGTATGAACCTTGAGGCTGCTGCCATTTTTCCACTTAACCA 2738
                                                                                                                                                                             1016 NNNYWIGWKIRWIAYRMAIRWMKAWWKVMAIGSWNINSYARWAYKIRAYKGWYYNACAWR 1075
                                                                                                                                                                                                             2854 AGAAAAAGTATGTATTGCATACTTAGTAGAATAGATCACAACATACAAATTCAATTCAGT 2913
                                   AACCAGCCTGAAGGTGAACCTCGAAACTTGTTTCATAAATCTTTCAA-----AAGTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDITOR TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/255,829
FILING DATE: 23-FEB-1999
PRIOR APPLICATION DATA:
PRILING DATE: 22-AUG-1997
PRIOR APPLICATION DATA:
PRILING DATE: 22-AUG-1997
PRIOR APPLICATION DATA:
PRILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/09255829
Patent No. 6461617
GENERAL INFORMATION:
APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IIOO NEW YORK AVENUE, NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1581,0130002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET UNBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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CORRESPONDENCE ADDRESS:
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1136 RYW 1138
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STRANDEDNESS:
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US-09-255-829-17
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1.7%; Score 54.8; DB 3; Length 3042;

Query Match

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2571 TTTTCAGCTTTCCAAATACGTAGATAATCAAAGATTATTATTATTACTGAATATAT 2630
                                                                    2258 TICTCAGTICAATGAAGCAATAATGAAGTATTTAACTCTTTCACTACAGTTCTTGCAAGT 2317
                                                                                                                            2391 ATGCTCTGTTTCATATTTAATGAATTCTATGATCCCTTATGGTGTTAAACGGTTAGAAGA 2450
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                                                                                                                                                                                                                   2435 CATATGTTCATTAAAAGCATAGCACTTTGAAATTAACTATAAAATAGCTCATATTTACA
   Gaps
   3,
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Indels
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APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
0; Mismatches 152;
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Sequence 2813, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
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SEQ ID NO 14222
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR APPLICATION NUMBER: 60/241,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASELSEQ for Windows Version 4.0
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241 KAWRASCMMRRKYAGKSKTSYKSMWMCWTRSWKYCYTKARWTGYYCYRKGGMWGKRGRWY 300
                                      301 ASKKYMWKRWWWGWARMYRYSTGTRASMWWRRWYTDMMKWWKYAWARAAWRWWAMWW 358
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1.7%; Score 53; DB 4; Length 88490;
Best Local Similarity 46.9%; Pred. No. 0.014;
Matches 202; Conservative 0; Mismatches 225; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12758, Application US/09949016
Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CRGANISM: Human
US-09-949-016-12758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 12758
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ADDICANT: VENTER, J. Craig et al.
ADDICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: 05/241, 755
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR FILING DATE: 2000-09-08
NUMBER: PARELIAND NUMBER: 60/231, 498
NENCH APPLICATION NUMBER: 60/231, 498
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US-09-710-279-4346

Sequence 4346, Application US/09710279

Sequence 4346, Application US/09710279

Patent No. 6703492

GENERAL INFORMATION:

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REFERENCE: PU3480US

CURRENT PAPLICATION NUMBER: US/09/710,279

CURRENT FILING DATE: 2000-11-09

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4346
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6.9%; Pred. No. 0.014;
ve 0; Mismatches 225; Indels
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Best Local Similarity 46.9%;
Matches 202; Conservative
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US-09-949-016-14222
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2258 TTCTCAGTTCAATGAAGCAATAATGAAGTATTTAACTCTTTCACTACAGTTCTTGCAAGT 2317
                    1131 İTİTGATĞCİAĞİCTİAAAGATGCATİAİTAAAGİATAİTAİĞATAATAGAGGAACTTT 1190
                                                                                                                                1191 AATTGGTCAAGTAGATAGATTAAAAGATAAAGTTAATAATACACTTAGTACAGATATACC 1250
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Pred. No. 0.0051;
0; Mismatches 144; Indels 3
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COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/255,829
FILING DATE: 23-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/02273
FILING DATE: 22-AUG-1997
PRIOR APPLICATION NUMBER: US 08/782,893
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C. 1100 NEW YORK AVENUE, NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09255829;
Patent No. 6461617;
GENERAL INFORMATION:
APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments;
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0130002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION TELEPHONE: 202-371-2600
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Best Local Similarity 50.77
Matches 151; Conservative
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STRANDEDNESS: double
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; LOCATION:
US-09-255-829-7
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                                                                                                                                                                                                                                                                                                                                  2342 GTATAATTGCCAGTCAGTCTCTTTATAGTGAGAAAATTTATTGGTTAGTAATATAAATAT 2401
                                                                                                                                                                                                                                                                                                                                                                                                                                              TITAAACTA-AATATATAAATCTATAATGTTAAACATATGTTCATTAAAA---GCATAGC 2457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2458 ACTTIGAAATTAACTATATAAATAGCTCATATTTACACTTACAGCTTTTCATTTGATCAG 2517
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APPLICANT: U.S. Army Medical Reseach Institute for Infectious Diseases
APPLICANT: John S. Lee
APPLICANT: Deter Bushko
APPLICANT: Peter Pushko
APPLICANT: Michael D. Parker
APPLICANT: Mark T. Dertabaugh
APPLICANT: Mark T. Dertabaugh
APPLICANT: Mark T. Dertabaugh
APPLICANT: Mark T. Dertabaugh
TITLE OF INVENTION: Botulinum Neurotoxin Vaccine
FILE REFERENCE: 003/124/5AP RILD 98-21
CURRENT APPLICATION NUMBER: US/09/350,756
CURRENT PILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                       416 GAATAATTAAGATCACAAATCTTAATATGGTGAATATTTAATGGTACCTAAAAAATAAAA 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      476 TTTAAACTACAATGTCTAAATCCATATGTTGTTTCATTAGAGGATTTAAAAATGATTATA 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     536 ACACTAAAAGATTTCAAATTATTATTTAATATAAAATTTACATATGATAAACGAATAAC 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  596 AATTCCAATATAAATTATTTTTTGATTATTTTTATTATAACTATATATTTTATAAAAA 655
                                                                                                                                                                                                                                                                                4; Gaps
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                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.6%; Score 51.6; DB 4; Length 1987;
50.7%; Pred. No. 0.0044;
tive 0; Mismatches 144; Indels 3.
                                                                                                                                                                                                                  Length 3404;
                                                                                                                                                                                                                  Score 52; DB 4; Length 340
Pred. No. 0.0046;
0; Mismatches 105; Indels
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Patent No. 6495143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Clostridium botulinum
                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                  Query Match
Best Local Similarity 56.0%;
                                                                                                                                                                                                                                                                          Matches 139; Conservative
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Best Local Similarity
                                                                                                                                            ; OTHER INFORMAT
US-09-710-279-4346
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LENGTH: 3404
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NAME/KEY:
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US-09-255-829-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: WAS
STATE: DO
COUNTRY:
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                                                                                                trirgardcriadrorriaaagargcarrarraaagrarararararaaragaggaactrr 2489
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COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPRES: PARCHIN Release #1.0, Version #1.30 (BPO)
SOFTWARE: PATECHIN Release #1.0, Version #1.30 (BPO)
SOFTWARE: PATECHIN ROLAS:
FILING DATE: 23-FEB-1999
PRIOR APPLICATION NUMBER: PCT/GB97/02273
APPLICATION NUMBER: PCT/GB97/02273
FILING DATE: 22-AUG-1997
PRIOR APPLICATION NUMBER: US 08/782,893
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESWOND, ROBERT W.
RESISTENCE/DOCKET NUMBER: 1581.0130002
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: LESWOND, ROBERT W.
FRIENCE/DOCKET NUMBER: 1581.0130002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Pred. No. 0.0051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Kaith Alan
ITILE OF INVENTION: Recombinant Toxin Fragments
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09255829 Patent No. 6461617 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                             2490 AATTGGTCAAGTAGATAGATTAAAGATAAAGTTAATAATACACTTAGTACAGATATACC 2549
                                                                                  2378 TITATIGGITAGIAATATAAAT---ATTITAAACTAAATATATAAATCTATAATGITAAA 2434
                                                                                                                                                                                                                                                                                                     2495 CTTACAGCTTTTCATTTGATCAGGTCTGAAATCTTTAGCACTTAAGGAAAATGACTAT 2552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
APPLICATION NUMBER: US/09/255,829
FILING DATE: 23-FEB-1999
PRIOR APPLICATION NUMBER: PCT/GB97/02273
FILING DATE: 22-AUG-1997
PRIOR APPLICATION NUMBER: US 08/782,893
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRANTON NUMBER: 1581.0130002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFONS: 202-371-2600
TELEFONS: 202-371-2600
TELEFONS: SEQUENCE THEORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/09255829
Patent No. 6461617
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 50.77
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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2378 ITTAITGGTIAGTAATATAAAT ---AITTTAAACTAAATATATAAAATCTATAAATGTTAAA 2434
                                           2435 CATATGTTCATTAAAAGCATAGCACTTTGAAATTAACTATAAATAGCTCATATTTACA 2494
                                                          2490 AATTGGTCAAGTAGATAAAAGTTAAAAGTTAATAATAATAATACTACTAGTACAGATATAAC 2549
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2370 ATGCTCTGTTTCATATTTTAATGATTCTATGATCCTTATGGTGTTAAACGGTTAGAGA 2429

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Search completed: July 2, 2005, 19:50:47 Job time : 518 secs

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2, 2005, 12:38:20 ; Search time 1635 Seconds (without alignments) 11607.762 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aad06010 Human neu	Abs56723 Human NAR	Adj57933 Human NAR	Adlé2788 Human ova	Adn05171 Antipsori	Ads74320 PRO83903	Abv29614 Human pro	Abv23741 Human pro	Aad06007 Human neu	Adj57931 Human NAR	Adr40144 Human Nar	Aah14905 Human cDN	Aah44173 Human gly	Adj57938 Rat NARC	Aba09667 Human bon	Aba09583 Human bon	Adj57947 Rat NARC	Aah07671 Human cDN	Aas23890 Human ova	Aah82447 Human ova
SUMMARIES	ID	AAD06010	ABS56723	ADJ57933	ADL62788	ADN05171	ADS74320	ABV29614	ABV23741	AAD06007	ADJ57931	ADR40144	AAH14905	AAH44173	ADJ57938	ABA09667	ABA09583	ADJ57947	AAH07671	AAS23890	AAH82447
	DB	4	œ	12	Ŋ	12	13	S	ഗ	4	12	13	4	4	12	S	Ŋ	12	4	4	ß
	* Query Match Length DB	3206	3206	3206	3499	5443	5443	3499	3498	2738	2738	2019	1803	1929	3381	2477	1978	2393	168	546	546
	% Query Match	100.0	100.0	100.0	98.8	98.8	98.8	98.7	98.3	77.4	77.4	63.0	56.2	53.0	45.9	43.9	42.9	30.9	19.8	15.2	15.2
	Score	3206	3206	3206	3166	3166	3166	3164.4	3152.4	2481.8	2481.8	2019	1803	1698.2	1471.2	1406	1376.4	991	633.4	486.4	486.4
	Result No.	٦	7	m	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20

Abv88538 Human col	Aah12646 Human cDN	Ach18980 Human adu	Ad142779 Human ova	Aas24002 Human ova	Aah82567 Human ova	Adi71235 Human ova	Adl36395 Human ova	Abv35865 Human pro	Abv44927 Human pro	Human	Human	Abl79391 Human ova	Aat24062 Human gen	Abv05894 Human pro	Aak61234 Human imm	Aak80690 Human imm	Aak79627 Human imm	Aai12461 Probe #23	Aba54169 Human foe	Aai33815 Probe #25	Aba43713 Human bre	Aba23914 Probe #23	Aak27880 Human bon	Aak02440 Human bra
ABV88538	AAH12646	ACH18980	ADL42779	AAS24002	AAH82567	ADI71235	ADL36395	ABV35865	ABV44927	ABV15063	ABL81385	ABL79391	AAT24062	ABV05894	AAK61234	AAK80690	AAK79627	AAI12461	ABA54169	AAI33815	ABA43713	ABA23914	AAK27880	AAK02440
9	4	σ	Ŋ	4	Ŋ	ß	Ŋ	Ŋ	Ŋ	Ŋ	9	9	~	Ŋ	4	4	4	4	4	4	4	4	4	4
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14	13	13.3	12	11	7	Ħ	11	10	10	10	σ'n	o,	60	α)	œ	7	7	ø	Ġ.	ø	ø	ý	ý	ý
469.4	444.6	427	414.8	365.6	365.6	363.4	363.4	326.6	326.6	326	296.4	291	285	271	265.2	236	236	208.4	208.4	208.4	208.4	208.4	208.4	208.4
21	22	23	24	25	56	23	88	59	9	31	32	33	34	35	36	37	38	33	9	11	42	£3	44	5
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ALIGNMENTS

RESULT 1

Human; neuronal apoptosis regulated candidate 16B; NARC 16B; cytostatic; chromosome mapping; gene therapy; antisense therapy; lung disorder; central nervous system disorder; apoptosis; spleen disorder; angina; tuberculosis; Goodpasture's syndrome; liver disorder; jaundice; infectious disorder; brain disorder; cerebral oedema; gonorrhoea; heart disorder; kidney disorder; glomerulonephritis; testes; virucide; epididymis disorder; amscle disorder; pancreatic disorder; diabetes; cytoprotectant; immunostimulant; tumour; antiinflammatory; antimicrobial; neuroprotective; gynaecological; ds. Human neuronal apoptosis regulated candidate (NARC) 16B DNA. AAD06010 standard; DNA; 3206 BP. (first entry) 31-JUL-2001 AAD06010; AAD06010

Homo sapiens.

WO200131007-A2.

03-MAY-2001.

20-OCT-2000; 2000WO-US029132.

(MILL-) MILLENNIUM PHARM INC.

99US-0161188P.

22-OCT-1999;

Chiang LW;

WPI; 2001-308641/32.

Rat brain polypeptides, nucleic acids and antibodies, useful for diagnosis and treatment of central nervous system disorders and disorders associated with aberrant apoptosis.

Claim 1; Page 148; 161pp; English.

The invention relates to human homologues of neuronal apoptosis regulated

cc candidate (NARC) nucleic acid molecules and proteins derived from rat brain and programmed cell death libraries. The nucleic acids of the invention are useful for assaying the presence of a nucleic acid molecule and for chromosome mapping. They are also used in gene therapy and and for chromosome mapping. They are also used in gene therapy and carrier and for chromosome mapping. They are also used in gene therapy and carrier and is not therapy and and for chromosome mapping. They are also used in gene therapy and contrain an intense therapy. The NARC sequences are useful for treating central contrain contraint and immune response and for isolating binding partners. Diseases treated include spleem disorders (e.g. tuberculosis and congestive congopasture's syndrome and bronchial asthma), liver disorders (e.g. faundice and hepatic failure), infectious disorders (e.g. viral companing disorders (e.g. cerebral oedema, hypertensive concephalopathy and hydrocephalus), heart disorders (e.g. cysts and splantand myocardial infarction), kidney disorders (e.g. cysts and slommerulonephritis), testes and epididymis disorders (e.g. cysts and syphilis), skeletal muscle disorders (e.g. tumours) and pancreatic disorders (e.g. pancreatic shuman apoptosis regulated candidate (NARC) 168 DNA \$

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er;	.3206; 0; Gaps	13 13 13 13 13 13 13 13 13 13 13 13 13 1	CCTCGCTCTCGGGCGGGGGGGGGGACCGGACCTGCGGACTAGCGAACCCGGAGCACG 	acatcataaaataaatccatcagaatgacaccttctcaggttgcctttgaaataagaga 	ACTCTTTTACCAGAGAAGTTTTTGCGATATGTGGAAGCTGTGATGCTTTGGGAAACTGG 	aaticctcaaaatgctgtggctcttcttccagagaatgacacaggtgaaagcatgctatgg 	aaagcaaccattgtactcagtagagagtatcagttcagt	TTTTTAGAACCAAAGACTATCGGTGGTCCATGTCAAGTGATAGTTCACAAGTGGGGAGACT 	CATCTACAACCACGATCAATAACCCCTTTAGAAAGCGAAATTATTGATGACGATGGACAA 	tttggaatccacaatggtgttgaactctggattctggatggctgacatgtcagactgaa 	ataagattacgtttgcattattctgaaaacctcctgtgtcaataaccaggaaaatta 	aaaaaatctagatttagggtgaagctgacactagaaggcctggaggaagatgacgatgat 	agggtatctcccactgtactccacaaaatgtccaatagcttggagatatcttaataagc
T; 0 U; 0 Other	DB 4; Length 0; Indels	GGCGCCCGGTAC	TGCGGACTAGCC TGCGGACTAGCG	TCAGGTTGCCTT	aaagctgtgatgc 	ATGACACAGGTGA 	rtcagtatcgctv rtcagtatcgctv	aagtgatagttoj aagtgatagttoj	GCGAAATTATTA' GCGAAATTATTA'	CTGGATGGCTGA(CTGGATGGCTGA(CTGTGTCAATAA CTGTGTCAATAA	AAGGCCTGGAGG 	atagettggaga
682 G; 956	Score 3206; Pred. No. 0; Mismatches	GGCACGGACGGC	GGCGACGCGGAC GGCGACGCGGAC	GAATGACACCTT	rttgcgatatgtg 	CTTCTTCCAGAGA 	agaggagtatcag agaggagtatcag	SGTGGTCCATGTC 	accctttagaaa accctttagaaa	SAAACTCTGGATT 	TCTGAAAACCTC TCTGAAAACCTC	aagctgacactag aagctgacactag	cacaaaatgtcg cacaaaatgtcg
988 A; 580 C;	0	GCGTCCGGGCGP	19929999999999999999999999999999999999	ATAAATCCATCA \ATAAATCCATCA	CCAGGAGAAGTTT 	AATGCTGTGGCTC AATGCTGTGGCTC	ATTGTACTCAGT/ ATTGTACTCAGT/	CCAAAGACTATCO	CCACGATCAATA CCACGATCAATA	CACAATGGTGTT CACAATGGTGTT	CGTTTGCATTAT CGTTTGCATTAT	AGATTTAGGGTG 	CCCACTGTACTC
sequence 3206 BP; 9	ry Match 100.0%; . Local Similarity 100.0%; thes 3206. Conservative	GTCGACCCAC											
sequence	ry Match	7	61	121	181	241	301	361	421	481	541	601	661

දු පු	721	721 GACAATGAGTTCAAGTGCAGGCATTCACAGCCGGAGTGTGGGGTTATGGCTTGCAGCCTGAT 780
ζō	781	CGTTCGACAGAGATACAGATGGAACCAGATAACCTGGAACTAATCTTTGAT 840
g G	781	CGTTGGACAGAGTACAGCATACAGATGGAACCAGATAACCTGGAACTAATCTTTGAT GTG
85 S	841	TTTTCGAAGAAGATCTCAGTGAGCACGTAGTTCAGGGTGATGCCCTTCCTGGACATGTG 900
ò	901	GGTACAGCTTGTCTTATCATCCACCATTGCTGAGAGTGGAAAGAGTGCTGGAATTCTT 960
QQ	901	GGTACAGCTTGTCTTATCATCCACCATTGCTGAGAGTGGAAAGAGTGCTGGAATTCTT 960
ò	961	ACTETTCCCATCATGAGGAGAATTCCCGGAAAACAATAGGCAAAGTGAGAGTTGACTAT 1020
Q Q	961	ACTCTTCCCATCATGAGCAGAAATTCCCGGGAAACAATAGGGAGAGTGAGT
& £	1021	ATAATTATTAAGCATTACCAGATACAGTTGTGAAATGTTCAAATCTTCAATTTTCCAAGTAI 1989
l &	1081	1140
Db	1081	TGGAAGCCAAGAATACCATTGGATGTTGGCCATCGAGGTGCAGGAAACTCTACAACAACT 1140
λõ	1141	GCCCAGCTGGCTAAAGTTCAAGAAAATACTATTGCTTCTTTAAGAAATGCTGCTAGTCAT 1200
q	1141	GCCCAGCTGGCTAAAGTTCAAGAAAATACTATTGCTTCTTTAAGAAATGCTGCTAGTCAT 1200
Š i	1201	GCTGCAGCCTTTGTAGAATTTGACGTACACTTTCAAAGGACTTTGTCCCGTGGTATAT 1260
g	1201	GCTGCAGCCTTTGTAGAATTTGACGTACACCTTTCAAAGGAACTTGGCCCCGGGGGAATTTTGACGTACTTTTTTTT
රු ද	1261	CATGRICTTACCTGTTGTTTGACTAFGAAAAGAAATTGATGCTGGTCGATCCAGTTGATTA 1320
9 8	1221	menca a a menca acta a a a a a a a a a a a a a a a a
δ 6	1321	TTGAAATTCCAGTAAAAGAATTAACATTTGACCAACTCCAGTTATAAAGCTCACTCA
ζ	1381	GIGACICCACIGAANICTAAGGATCGGAAGAATCIGIGGTTCAGGAGAAAATTCCITT 1440
qq	1381	GTGACTGCACTGAAATCTAAGGATCGGAAAGAATCTGTGGTTCAGGAAGAAATTCCTTT 1440
δ	1441	TCAGAAAATCAGCCATTTCCTTCTCTTAAGAIGGTTTTAGAGTCTTTGCCAGAAGATGTA 1500
DP	1441	rcadaaaarcadccartrccrrcrraagarggrrrragagrcrrggcagaagargra 1500
ò	1501	GGGTTTAACATTGAAATAAAATGGATCTGCCAGCAAAGGGATGGAATGTGGGATGGTAAC 1560
Ωp	1501	GGGTTTPACATTGAAATAAAATGGATCTGCCAGCAAAGGGAATGGAATGTGGGAATGGAAACGGAAAGGAAAGGAAAGGAAAAGGAAAAGGAAAAGGAAAAGAAAA
ò	1561	TTATCAACATATTTTGACATGAATCTGTTTTGGGATAAATTTTAAAAACTGTTTGGGATACCA
Db	1561	TTATCAACATATTTTGACATGAATCTGTTTTTGGATATAATTTTAAAAACTGTTTTAGAA 1620
ζ	1621	AATTCTGGGAAGAGGAGAATAGTGTTTTCTTCATTTGATGCAGATATTTGCACAATGGTT 1680
ДQ	1621	AATTCTGGGAAGAGAGAATAGTGTTTTCTTCATTTGATGCAGATATTTGCACAATGGTT 1680
ò	1681	CGGCAAAAGCAGAACAAATATCGATACTATTTTAACTCAAGGAAAATCTGAGATTTAT 1740
Dp	1681	. CGGCAAAAGCAGAACAATATCCGATACTATTTTTAACTCAAGGAAAATCTGAGATITAT 1740
<i>\</i> 6	1743	CCTGAACTCATGGACCTCAGATCTCGGACAACCCCCATTGCAATGACTTTTCACAGTTT 1800
අු	174]	. CCTGAACTCATGGACCTCAGATCTCGGACAACCCCCATTGCAATGAGCTTTGCACAGIII 1800
λ̈	180	

B & B & B & B & B & B & B

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\$ 6 6 6

2881 AGAATAGATCACAACATACAATTCAATTCAGTGCTTTAGGTGTTAAGCATGAGAT 2940 2941 TGTACATGTTACTGTTAGGTCCTTGCATCTGTGGTGCTAGGTGAGTATGAGAAGATCT 3000 2941 TGTACATGTTACTGTTAGGTCCTTGCATCTGTGGTGAGTATGAGAAGATGTC 3000 3001 AAGGACTGGACGTTTTTGTTGCCTAAAAAAAAAAAAAAA	ABSS6723 standard; CDNA; 32 ABSS6723; 24-FEB-2003 (first entry) Human NARC16 cDNA. NARC10; NARC16; cytostatic; antiinflammatory; nephrotron inflammosuppressive; thyromim tranquiliser; neuroleptic; AIDS: cell cycle disruption viral infection; nucleosome cell cycle regulation; canc p53 mutation; graft rejecti autoimmune disorder; valvul systemic lupus erythematosu immune—mediated glomerulone acquired immunodeficiency s Alzheimer s disease; parkin spinal muscular atrophy; re myelodysplastic syndrome; i reperfusion injury; liver di ischaemic cardiomyopathy; myelodysplastic syndrome; c senile dementia; Huntington severe bipolar affective di Homo sapiens. Key Location/Qu T+tag= a //ttag= a //ttag= a //ttag= a //ttag= a //ttag= a //ttag= a //ttag= a //ttag= a //ttag= a //ttag= a	16-JAN-2001; 2001US-0262306P. 15-JAN-2002; 2002US-00047855. (MILL-) MILLENNIUM PHARM INC.
8 6 8 6 8 6 8 6 8		R K X X
	TAGTITITATICGCAGAGGCCATTICGGGGCGCGCCCCCCCCCTCTCGGGTATTCATT TAGTITITATICGCACAGAGGCCATTICGGGGCGCGCCCCCCCCCTCTCGGGTATCATT TAGTITITATICGCACAGAGGCCATTICGGGGCGCGCCCCCCCCCTCTCTGGGTATCATT TAGTITITATICGCACAGAGGCCATTCTGGCGCACTCATTCATCATTT TCATCACCACAGACCATTCATCATCATCATCTCTCACTCA	CTGCAGGGTAATTTAATGTATAAAATATTAGTAAGAAAAAGTATGTATTGCATACTTAGT AGAATAGATCACAACATACAAATTCAATTC

8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

WPI; 2003-058503/05.

P-PSDB; ABB84606.

Novel isolated programmed cell death-related polypeptide, NARC10 and NARC16, useful for treating disorders associated with abnormal apoptotic process e.g. Alzheimer's disease, cancer, myocardial infarction, stroke.

Claim 1; Fig 4A-C; 123pp; English

This invention describes novel cell death-related polypeptides NARC10 and NARC16, located on chromosome 4q11-4q21 and which have cardiant, antiHIV, mannosuppressive, dermatological, antiHiffammatory, crebipoprotective, concurred to concurred to the concurred to concurred to the concurred to concurred to the concurred to manunosuppressive, cytostatic; thyromimetic, nephrotropic, antidabetic, immunosuppressive, cytostatic; thyromimetic, nephrotropic, antidabetic, immunosuppressive, cytostatic; thyromimetic, nephrotropic, concurred to manuostimulant, tranquiliser, hypotensive and concurred to map NARC genes on a chromosome, e.g. to locate gene invention can be used to madulate NARC10 or NARC16 polymelectides, to map NARC genes on a chromosome, e.g. to locate gene cregions associated with genetic disease or to associate NARC10 or NARC16 with a disease. The polypeptides are also useful for modulating the apportant process, and are therefore useful for modulating and treating disorders associated with increased apoptosis, inhibition of apoptosis or disruptions in cell cycle, for regulating cellular functions including process, and care despendent tumours, uncommune disorders cell cycle. Preferably, the products of the invention are useful for treating disorders associated with abnormally low rate or abnormally high creating disorders associated with abnormally low rate or abnormally high are of apoptosis e.g. concress including follicular lymphomas, crinomas crincluding systemic lupus erythematosus, diabetes, graft rejection, infections caused by herpes viruses, virus-induced infections e.g. infections caused by herpes viruses, virus-induced infections e.g. infections caused by herpes viruses, virus-induced infections e.g. infections caused by herpes viruses, virus-induced concurred infections caused by herpes viruses, virus-induced infections, stroke and repertusion injury), and toxin (e.g. allocated and repertusion), myelodysplastic syndromes cardiomyopathy and valvular heart disease, and carebellar dependence of i disorders, senile dementia, Huntington's disease, hypertension, schizophrenia, attention deficit disorder, mania, anxiety, severe bipolar affective disorder (BP-I). This sequence encodes the human NARC16 protein described in the method of the invention

Sequence 3206 BP; 988 A; 580 C; 682 G; 956 T; 0 U; 0 Other;

240 120 120 180 121 ACATCATAAAATAAATCCATCAGAATGACACCTTCTCAGGTTGCCTTTGAAATAAGAGA 180 240 AATCCTCAAAATGCTGTGGCTCTTCTTCCAGAGAATGACACAGGTGAAAGCATGCTATGG 300 9 9 61 corcecratices de consecuenc ACATCATAAAATAAATCCATCAGAATGACACCTTCTCAGGTTGCCTTTGAAATAAGAGA **ACTCTTTTACCAGGAGAAGTTTTTGCGATATGTGGAAGCTGTGATGCTTTTGGGAAACTGG** GTCGACCCCACGCGTCCGGGCGAGGCACGGCGGGGGGCGCCCGGTACCTCTGCCCGGGT gregacecaceceaeceaeceaecaceaeceaeceaececececeeraecereceer Gaps ö DB 8; Length 3206; Indels ö 100.0%; Score 3206; 100.0%; Pred. No. 0; tive 0; Mismatches Best Local Similarity 100. Matches 3206; Conservative 241 121 181 Query Match

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λ	301	AAAGCAACCATTGTACTCAGTAGAGGAGTATCAGTTCAGTATCGCTACTCCAAAGGGTAC 360
qq	301	AAAGCAACCATTGTACTCAGTAGGAGTATCAGTTCAGTATCGCTACTTCAAAGGGTAC 360
ò	361	TTTTTAGAACCAAAGACTATCGGTGGTCCATGTCAAGTGATAGTTCACAAGTGGAGACT 420
අු	361	TTTTTAGAACCAAAGACTATCGGTGGTCCATGTCAAAGTCAAAGTCACAAGTGAAAGTCACAAGAACT
දු සි	421	CATCTACAACCACCATCAATAACCCCTTTAGAAGGGAAATTATTATTATTGACATGACAAAA 480
λ	481	TTTGGAATCCACAATGGTGTTGAAACTCTGGATTCTGGATGGCTGACATGTCAGACTGAA 540
Db	481	TITGGAAICCACAAIGGIGITGAAACICIGGAITGIGGIGCTGGCIGACAIGICAGAA 540
λ	541	ATARGATTACGTTTGCATTATTCTGAAAAACCTCCTGTGTCAATAACCAAGAAAAATTA 600
qq	541	ATAAGATTACGTTTGCATTATTCTGAAAAACCTCCTGTGTCAATAACCAAGAAAAATTA 600
8 8	601	SOI AAAAATCTAGATTTAGGGTGAAGCTGACACTAGAAGGCCTGGAGGAAGATGATGTGT 660
3 8	661	AGGGTATCTCCCACTGTACTCCACAAAATGTCCAATAGCTTGGAGATATCCTTAATAAGC 720
. d	661	
ò	721	GACAAIGAGITCAAGIGCAGGGTTCACAGCCGGAGTGTGGTTATGGCTTGCAGCCTGAT 780
qq	721	GACAATGAGTTCAAGTGCAGGCATTCACAGCCGGAGTGTGGTTATGGCTTGCAGCCTGAT 780
λŏ	781	CGTTGGACAGAGTACAGCATACAGACGATGGAACCAGATAACCTGGAACTAATCTTTGAT 840
qq	781	CGTTGGACAGAGTACAGCATACAGACGATGGAACCAGATAACCTGGAACTAATCTTTGAT 840
δλ	841	TITITCGAAGAACTCTCAGTGAGCACGTAGTTCAGGGGAGTGCCCTTCCTGGACATGTG 900
qq	841	TITICGAAGAAGATCICAGIGAGCACGIAGIICAGGGGAGAIGACCCIICCTGGACAIGIG 900
ζ	901	GGTACAGCTIGICTCTIAICAICCACCAITGCIGAGAGTGGAAAGAGTGCTGGAATICTI 960
qq	901	GGTACAGCTTGTCTTTATCATCCACCATTGCTGAGAGTGGAAAGAGTGCTGGAATTCTT 960
λΌ	961	ACTCTTCCCATCATGAGCAGAAATTCCCGGAAACAATAGGCAAAGTGAGAGTTGACTAT 1020
Ωp	961	ACTCTTCCCATCATGAGCAGAAATTCCCGGAAACAATAGGCAAAGTGAGGTTGACTAT 1020
ογ	1021	ATAATTATTAAGCCATTACCAGATACAGTTGTGACATGAAATCTTCATTTTCCAAGTAT 1080
Db	1021	ATAATTATTAAGCCATTACCAGGATACAGTTGTGACATGAAATCTTCATTTTCCAAGTAT 1080
δγ	1081	TGGAAGCCAAGAATACCATTGGATGTTGGCCATCGAGGTGCAGGAACTCTACAACAACT 1140
ΩÞ	1081	rgsaagccaagaaraccarrgaargrrggccarcgaggrgcaggaaacrcracaacaacr 1140
δλ	1141	GCCCAGCTGGCTAAAGTTCAAGAAAATACTATTGCTTCTTTAAGAAATGCTGCTAGTCAT 1200
Д	1141	GCCCAGCTGCCTAAAGTTCAAGAAATACTATTGCTTCTTTAAGAAATGCTGCTAGTCAT 1200
à	1201	GGIGCAGCTITIGIAGAAIITGACGIACACCTITCAAAGGACTITGIGCCCGTGGIATAT 1260
Db	1201	GGIGCAGCCTTTGTAGAATTTGACGTACACCTTTCAAAGGACTTTGTGCCCGTGGTATAT 1260
δλ	1261	CAIGATCTTACCTGTTGTTTGACTATGAAAAGAAATTTGATGCTGATCCAGTTGAATTA 1320
QQ	1261	CATGATCTTACCTGTTGTTTGACTATGAAAAGAAATTTGATGCTGATCCAGTTGAATTA 1320
ò	1321	
qq	1321	TTIGAAATTICCAGTAAAAGAATTAACATTIGACCAACTICCAGTIGITAAAAGCTCACTCAT 1380

2461	y 2521 TGAAATCTTTAGCACTTAAGGAAAATGACTATGCATAATTATACCTGACCATGAAAAAA 2580	y 2581 TAAGTACCTCAAATGCATGGACTGGTGATTCCAACTGCACAAATCTTGTGCCA 2640 2581 TAAGTACCTCAAATGCATTTGCACTGGTGATTCCAACTGCACAAATCTTTGTGCCA 2640	y 2641 TCTTGTATATAGGTATTTTTACATGGGTTGACATGCACACACA	y 2701 ATGAACCTTGAGGCTGCTGCCATTTTTCCACTTAACCAAACCAGCCTGAAGGTGAACCTC 2760 2701 ATGAACCTTGAGGCTGCTGCCATTTTTCCACTTAACCAAACCAGCCTGAAGGTGAACCTC 2760	2761	y 2821 CTGCAGGGTAATTTAATGTATAAATATTAGTAAGAAAAAGTATGTATTGCATACTTAGT 2880 [y 2881 AGAATAGATCACAACATACAAATTCAGTGCATGCTTTAGGTGTTAAGGTGTGAGGT 2940	y 2941 IGTACATGTTACTGTTAGGTCCTTGCATCTGTGGTGCTAGGTGAGAAGATGTC 3000 2941 IGTACATGTTACTGTTAGGTCCTTGCATCTGTGGTGCTAGGTGAGAAGATGTC 3000	y 3001 AAGACTGGACGTATTTGTTGCCTAAAAAAAAGGCTGTTTGTAGGCGTTTTAAATAT 3060	y 3061 GCTTATTTGTGTGTCTCACTACTACACACTGTTGCTTTGTGGGTTTGTTT	y 3121 ATGTGCGTGTGTTATACAGTAGATTTCCATGCAGAAAATTAAATGTCCTGAATTCT 3180	y 3181 Caaraaaaaaaaaaagggggggg 3206 	RESULT 3 ADJ57933 ID ADJ57933 standard; cDNA; 3206 BP.	X ADJ57933; X T 06-MAY-2004 (first entry)		lung disease; cirrhosis; hepatitis; atherosclerosis; myocardial infarction; inflammation; anaemia; glomerulone osteoporosis; AIDS; acquired immunedeficiency syndere; Parkinson's disease; Alzheimer's disease; stroke; dermati		
qa	S G	& 8	상 옵	& a	oy ag	S G	& 4g	장 점	A A	& 8	& 8	& B	A P	iakk K	## # # #	K K K	222 X	8 X
	<u> </u>														 .		v-	
1381 GTGACTGCACTGAAATCTAAGGATCGGAAAGAATCTGTGGTTCAGGAGGAAAATTCCTTT	aagatgta aagatgta	ATGGTAAC	TTTTAGAA TTTAGAA	1621 AATTCTGGGAAGAGAGAATAGTGTTTTCTTCATTTGATGCAGATATTTGCACAATGGTT	AGATTTAT AGATTTAT	171 CTGAACTCATGGACCTCAGATCTCGGACAACCCCCATTGCAATGAGCTTTGCACAGTTT	1801 GAAAATCTACTGGGGATAAATGTACATACTGAAGACTTGCTCAGAAACCCATCCTATATT 1860	ATGATCCT		GATTGGATGCCTGAACAACAATATATTCCAAGTGGAGCAATTGGAACGCCTGAAGCAG 	GAATTGCCAGAGCTTAAGAGCTGTTTGTGTCCCACTGTTAGCCGCTTTGTTCCCTCATCT	GAATGCT GAATGCT	2161 TAGTITITATICCACAGAGGICALTITGCGGGCGTGCACCGCTGTTCTGGGTATTCATTT 2220	2221 ITCATCACTAGACATTGTTGATCTATGCCTTTTGGGCTTCTCAGTTCAATGAAGCAATAA 2280 	2281 IGAAGTAITTAACTCTTTCACTACAGTTCTTGCAAGTATGCTAITTAAATTACTTGGCCA 2340 	2341 GGTATAATTGCCAGTCAGTCTCTTTATAGTGAGAAAATTTATTGGTTAGTAATATAAATA 2400 	2401 TITTAAACTAAATATATAAATCTATAAAGATATGTTCATTAAAAGCATAGGCT 2460 .	TCAGGTC

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GGTGCAGCCTTTGTAGAATTTGACGTACACCTTTCAAAGGACTTTGTGCCCGTGGTATAT 1260
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TTTTTAGAACCAAAGACTATCGGTGGTCCATGTCAAGTGATAGTTCACAAGTGGGAGACT
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                                                                    AAAGCAACCATTGTACTCAGTAGGAGTATCAGTTCAGTATCGCTACTTCAAAGGGTAC
                                                                                                                                                        TTTTTAGAACCAAAGACTATCGGTGGTCCATGTCAAGTGATAGTTCACAAGTGGGAGACT
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Chiang LW, Hunter JJ;
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100.0%; Pred. No. 0;
ative 0; Mismatches
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99US-0161188P.
2000US-018517P.
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2002US-00284014.
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Matches 3206; Conservative
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20-OCT-2000; 2
31-GAN-2001; 2
28-FEB-2001; 3
31-OCT-2001; 2
25-MAR-2002; 2
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30-OCT-2002;
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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
  21-MAR-2000; 2000US-0191031P.
25-MAY-2000; 2000US-0207124P.
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25-JUL-2000; 2000US-0220661P.
21-DEC-2000; 2000US-0257672P.
                                               WPI; 2001-611502/70.
                                       Lee J,
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The invention relates to nucleic acid markers which are overexpressed in covarian cancer cells as compared to their expression in normal (i.e. noncarcian cancer cells as compared to their expression in normal (i.e. noncaced by the markers, antibodies that selectively bind to the encoded by the markers, antibodies that selectively bind to the cenceded by the markers, antibodies that selectively bind to the corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention and a method of treating a corresponding to a marker objectively to a marker of the patient antisense objigonuclectide complementary to a marker of the invention. The marker in a patient sample and a normal level of expression of the marker in a patient sample and a normal level of expression of the marker in a patient sample and a normal level of expression of the marker corresponds to a secreted protein or to a transcribed of septent of the presence of protein or protein fragment to secreted protein or to a transcribed corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment is assessed by detecting the presence of corresponding to the marker. The presence of corresponding to the marker or anneals with the marker or anneals with the marker or anneals with the marker or anneals with the marker or anneals with a portion of the polynucleotide which anneals with the marker or anneals with a patient comparing the level of expression of the marker is a subsequent time, repeating the method at a subsequent time and comparing the level of expression of the marker is a goused for monitoring the method of ovarian cancer in a patient which involves detecting the presence of polynucleotide which anneals with the marker or an anneal with a portion of time and comparing the level of expression of the marker or an anneal of the marker of Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer. Sequence 3499 BP; 1104 A; 610 C; 736 G; 1039 T; 0 U; 10 Other; Disclosure; SEQ ID NO 21000; 106pp; English.

Gaps .; 0 Length 3499; 5; Indels . 2 8 Score 3166; DB; Pred. No. 0; 0; Mismatches 98.8%; 99.8%; Matches 3169; Conservative Best Local Similarity 디 Query Match

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                                                                                                                                                                                     The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAAGACTATCGGTGGTCCATGTCAAGTGATAGTTCACAAGTGGGAGACTCATCTACAAC
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                                          Wood
                                                                                                                New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis
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                                           Schoenfeld J,
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                                                                                                                                                                 Claim 1; SEQ ID NO 1565; 3069pp; English
                                            Jackman J,
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                      GENENTECH INC
                                                                              WPI; 2004-305105/28.
P-PSDB; ADN05172.
                                            Clark H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO83903; Crohn's disease; rheumatoid arthritis; gastrointestinal-gen.; antirheumatic; antiarthritic; psoriasis; antipsoriatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating psoriasis, Crohn's disease, Ulcerative Colitis, or rheumatoid arthritis.
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                ACAACATACAAATTCAATTCAGTGCATGCTTTAGGTGTTAAGGATGAGATTGTACATGTT
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550 550 610 610 670 670 730 730 790 790 850 850 ö 310 430 490 250 310 TIGIACTCAGIAGAGGAGTATCAGTICAGTATCGCTACTICAAAGGGTACTTTTAGAAC 370 430 490 130 130 190 190 250 from healthy donors. It is also down-regulated 1.5-fold upon activation of CD4 T cells with CD28 or ICAM and down-regulated 2-fold upon activation of monocytes with LPS. PROB3903 can be used in a claimed method of identifying a compound that inhibits expression of the gene encoding it. The candidate compound is especially an antisense nucleic acid. The PRO POLYPEPTIGE, its antagonist or an antibody that binds the polypeptide are used in claimed methods for the alleviation or diagnosis of rhemautoid arthritis. Crohn's disease and psoriasis. A vector comprising the present nucleic acid can be used to transform a host cell, especially a CHO cell, Escherichia coli or yeast, for production of the PRO polypeptide. 70 AGTACAGCATACAGACGATGGAACCAGATAACCTGGAACTAATCTTTGATTTTTTCGAAG CCACTGTACTCCACAAAATGTCCAATAGCTTGGAGATATCCTTAATAAGCGACAATGAGT TCAAGTGCAGGCATTCACAGCCGGAGTGTGGTTATGGCTTGCAGCCTGATCGTTGGACAG ACAATGGTGTTGAAACTCTGGATTCTGGATGGCTGACATGTCAGACTGAAATAAGATTAC GTTTGCATTATTCTGAAAAACCTCCTGTGTCAATAACCAAGAAAAATTAAAAAATCTA GATTTAGGGTGAAGCTGACACTAGAAGGCCTGGAGGAAGATGACGATGATAGGGTATCTC ATGCTGTGGCTCTTCTTCCAGAGAATGACACGGGGAAAGCATGCTATGGAAAGCAACCA CAAAGACTATCGGTGGTCCATGTCAAGTGGTTCACAAGTGGGAGACTCATCTACAAC CACGATCAATAACCCCTTTAGAAAGCGAAATTATTATTGACGATGGACAATTTGGAATCC ATAAATCCATCAGAATGACACCTTCTCAGGTTGCCTTTGAAATAAGAGGAACTCTTTTAC CAGGAGAAGTTTTTGCGATATGTGGAAGCTGTGATGCTTTGGGAAACTGGAATCCTCAAA caggagaagriririgegarareregaagcreregarecririggaaacregaarecreaaa CAAAGACTATCGGTGGTCGTCTCAAGTGATAGTTCACAAGTGGGAGACTCATCTACAAC GCGTCCGGGCGAGGCACGGCGGGCGCCCGGTACCTCTGCCCGGCGGTCCTCGCTCTC Gaps Seguence 5443 BP; 1544 A; 1034 C; 1149 G; 1716 T; 0 U; 0 Other; ö Length 5443; Indels DB 13; ر. ک 98.8%; Score 3166; D 99.8%; Pred. No. 0; iive 0; Mismatches 0; Query Match 98.8 Best Local Similarity 99.8 Matches 3169; Conservative 671 191 371 431 551 551 611 611 671 731 731 191 131 251 311 311 371 431 491 491 191 191 251 71 131 11 7 8 8 8 8 8 8 g 8 8 g ò 8 8 8 8 8 8 B g ठे a 8 8 8 8 ò g ઠ

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1810 1750 1750 1810 1450 1450 1510 1570 1570 1690 1270 1330 1210 1270 1030 1030 1090 1150 1210 970 TGGGGATAAATGTACATACTGAAGACTTGCTCAGAAACCCATCCTATATTCAAGAGGCAA AAGCTAAGGGACTAGTCATATTCTGCTGGGGTGATGATACCAATGATCCTGAAAACAGAA AGAGGAGAATAGTGTTTTCTTCATTTGATGCAGATATTTGCACAATGGTTCGGCAAAAGC AGAACAAATATCCGATACTATTTTAACTCAAGGAAAATCTGAGATTTATCCTGAACTCA TGGACCTCAGATCTCGGACAACCCCCATTGCAATGAGCTTTGCACAGTTTGAAAATCTAC regaccreagarcregacaacccccarrecaargagcrrrgcacagrrrrgaaarcrac agaggagaatagtgttttttttattgatgcagatatttgcacaatggttcggcaaaagc CCTGTTGTTTTGACTATGAAAAAAAAATTTGATGCTGATCCAGTTGAATTATTTGAAATTC TGAAATCTAAGGATCGGAAAGAATCTGTGGTTCAGGAGAAAATTCCTTTTCAGAAAATC AGCCATTTCCTTCTTTAAGATGGTTTTAGAGTCTTTGCCAGAAGATGTAGGGTTTAACA TTGAAATAAAATGGATCTGCCAGCAAAGGGATGGAATGTGGGATGGTAACTTATCAACAT ATTTTGACATGAATCTGTTTTTGGATATAATTTTAAAAACTGTTTTAGAAAATTCTGGGA TTGTAGAATTTGACGTACACCTTTCAAAGGACTTTGTGCCCGTGGTATATCATGACTTA ccrerricarcrargaaaagaaarrrgargcrgarccagrrgaarrarrrgaarrc TCATGAGCAGAAATTCCCGGAAAACAATAGGCAAAGTGAGAGTTGACTATATAATTATTA AGCCATTACCAGGATACAGTTGTGACATGAAATCTTCATTTTCCAAGTATTGGAAGCCAA CTAAAGTTCAAGAAAATACTATTGCTTCTTTAAGAAATGCTGCTAGTCATGGTGCAGCCT GTCTCTTATCATCCACCATTGCTGAGAGTGGAAAGAGTGCTGGAATTCTTACTCTTCCCA GAATACCATTGGATGTTGGCCATCGAGGTGCAGGAAACTCTACAACAACTGCCCAGCTGG

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (d) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; carcinogen; pharmacodyanamic marker; gene; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
CGTATTTTGTTGCCTAAAAAAAAAGGCTGTTTGTAGGCGTTTTAAATATGCTTATTTG
                                                                                                   11 GCGTCCGGGCGAGGCACGGCGCGCCCCGGTACCTCTGCCCGCGGTCCTCGCTCTC
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                                                                                                                                                                                                Sequence 3499 BP; 1104 A; 609 C; 736 G; 1040 T; 0 U; 10 Other;
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99.8%; Pred. No. 0;
cive 0; Mismatches 6;
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CTGAACAACCAAATATATTCCAAGTGGAGCAATTGGAACGCCTGAAGCAGGAATTGCCAG GGAAATTGAAGGAACTTGGAGTTAATGGTCTAATTTATGATAGGATATATGATTGGATGC AGCCATTTCCTTCTTAAGATGGTTTTAGAGTCTTTGCCAGAAGATGTAGGGTTTAACA AGAACAAATATCGGATACTATTTTTAACTCAAGGAAAATCTGAGATTTATCCTGAACTCA AAGCTAAGGGACTAGTCATATTCTGCTGGGGTGATGATACCAATGATCCTGAAAACAGAA CCTGTTGTTTGACTATGAAAAAAAATTTGATGCTGATCCAGTTGAATTATTTGAAATTC 1347 CCTGTTGTTTGACTATGAAAAAGAAATTTGATGCTGATCCAGTTGAATTATTTGAAATTC

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                cytostatic; carcinogen; pharmacodyanamic gene; ss.
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 Human prostate expression marker cDNA 23732.
                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 4356-4357; 11750pp; English
                                                                                                                                                                                                                                                                                                                       WO, Mohahan JE;
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2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
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                                                                                                                                                            2001WO-US005171
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                               Human; prostate cancer;
pharmacogenomic marker;
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nucleic acids and antibodies, useful for of central nervous system disorders and disorders

associated with aberrant apoptosis.

Rat brain polypeptides, diagnosis and treatment WPI; 2001-308641/32

99US-0161188P.

22-OCT-1999;

(MILL-) MILLENNIUM PHARM INC.

Chiang LW;

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                                                                       2666 AAATGCATGCATTTGCACTGGTGATTCCAACTGCACAAATCTTGTGGCCATCTTGTATAT
                                                                                                                                                                                             2786 AGGCTGCCATTTTTCCACTTAACCAACCAGCCTGAAGGTGAACCTCGAAACTTGTT
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20-OCT-2000; 2000WO-US029132

WO200131007-A2

03-MAY-2001

Homo sapiens

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The invention relates to human homologues of neuronal apoptosis regulated candidate (NARC) nucleic acid molecules and proteins derived from rat brain and programmed call death libraries. The nucleic acids of the invention are useful for assaying the presence of a nucleic acid molecule and for chromosome mapping. They are also used in gene therapy and antisense therapy. The NARC sequences are useful for treating central nervous system disorders and disorders involving aberrant apoptosis, for inducing an immune response and for isolating binding partners. Diseases treated include spleen disorders (e.g. tuberculosis and congestive splenomegaly), lung disorders (e.g. qualt respiratory distress syndrome, Goodpasture's syndrome and bronchial atthma), liver disorders (e.g. jaundice and hepatic failure), infectious disorders (e.g. viral bepatitis), brain disorders (e.g. cerebral oedema, hypertensive encephalopathy and hydrocephalus), heart disorders (e.g. theoretic or signer and myocardial infarction), kidney disorders (e.g. pancreatic syphilis), skeletal muscle disorders (e.g. tumours) and pancreatic clasorders (e.g. pancreatics and diabetes). The present sequence is human neuronal apoptosis regulated candidate (NARC) 9B DNA
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us-10-047-855-4.rng

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Neuronal apoptosis regulated candidate; NARC; diagnosis; cancer; lung disease; cirrhosis; hepatitis; atherosclerosis; myocardial infarction; inflammation; anaemia; glomerulonephritis; osteoporosis; AIDS; acquired immunedeficiency syndrome; Parkinson's disease; Alzheimer's disease; stroke; dermatitis; drug screening; gene therapy; cytostatic; hepatotropic; nootropic; cerebroprotective; dermatological; virucide; neuroprotective; phosphatidylglycerolphosphate synthase; PGP synthase; human; ss.
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22-OCT-1999; 99US-0161188P.
31-JAN-2000; 200US-00495823.
28-FEB-2000; 200US-00495823.
31-JAN-2001; 200US-0073426.
31-JAN-2001; 200US-00773426.
31-OCT-2001; 200US-035037P.
31-OCT-2001; 200US-035037P.
31-OCT-2002; 2002US-0029662.
30-OCT-2002; 2002US-00229662.
30-OCT-2002; 2002US-00229662.
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Kapeller-Libermann R, Meyers
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ai F, Rudolph-Owen LA; Chiang LW, Hunter JJ;

New isolated nucleic acid molecules and polypeptides (e.g. 27411, 23413, 22438, 23553, NARC SCI or NARC 1) useful for diagnosing, preventing or treating disorders associated with the protein, e.g. cancer,

Claim 1; SEQ ID NO 32; 260pp; English.

The present invention provides isolated nucleic acid molecules and proteins designated 27411, 23413, 22438, 23551, 25278, 26212, NARC 102, NARC 103, NARC 11, NARC 113, NARC 15, NARC 25, NARC 3, NARC 4, NARC 11, NARC 113, NARC 15, NARC 19, NARC 26, NARC 27, NARC 28, NARC 29, NARC 20

Sequence 2738 BP; 880 A; 450 C; 540 G; 868 T; 0 U; 0 Other;

77.4%; Score 2481.8; 99.7%; Pred. No. 0; 0; Mismatches

Best Local Similarity >>., Matches 2486; Conservative

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751 99 CCAATAGCTTGGAGATATCCTTAATAAGCGACAATGAGTTCAAGTGCAGGCATTCACAGC 692 ŝ 셤 δ

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1111 1171 1231 1291 1411 1471 1026 1771 1051 1351 1531 1591 1651 TITIAACTCAAGGAAAATCTGAGATTTATCCTGAACTCATGGACCTCAGATCTCGGACAA 1086 546 999 CATTTGATGCAGATATTTGCACAATGGTTCGCCAAAAGCAGAACAAATATCCGATACTAT 1711 CCCCCATTGCAATGAGCTTTGCACAGTTTGAAAATCTACTGGGGATAAATGTACATACTG 1146 1147 AAGACTTGCTCAGAAACCCATCCTATATTCAAGAGGGAAAAGCTAAGGGACTAGTCATAT 1206 366 486 126 931 246 991 306 426 909 726 786 846 906 996 AGAAATTTGATGCTGATCCAGTTGAATTATTTGAAATTCCAGTAAAAGAATTAACATTTG 67 CGGAGTGTGTTATGGCTTGCAGCCTGATCGTTGGACAGAGTACAGCATACAGACGATGG CTGAGAGTGGAAAAGAGTGCTGGAATTCTTACTCTCCCATCATGAGAGAAAATTCCCGGA ATCGAGGTGCAGGAAACTCTACAACAACTGCCCAGCTGGCTAAAAGTTCAAGAAAATACTA 487 TIGCTICTITAAGAAATGCTGCTAGTCATGGTGCAGCCTTTGTAGAATITGACGTACACC TTTCAAAGGACTTTGTGCCCGTGGTATATCATGATCTTACCTGTTTTGACTATGAAAA ACCAACTCCAGTTGTTAAAGCTCACTCATGTGACTGCACTGAAATCTAAGGATCGGAAAG **AATCTGTGGTTCAGGAGGAAAATTCCTTTTTCAGAAAATCAGCCATTTCCTTCTCTTAAGA** AACCAGATAACCTGGAACTAATCTTTTGATTTTTTCGAAGAAGATCTCAGTGAGCACGTAG TTCAGGGTGATGCCCTTCCTGGACATGTGGGTACAGCTTGTCTTTATCATCCACCATTG CTGAGAGAGGAAAAAGAGTGCTGGAATTCTTACTCTTCCCATCATGAGCAGAAATTCCCGGA **AAACAATAGGCAAAGTGAGAGTTGACTATATAATTATTAAGCCATTACCAGGATACAGTT** GTGACATGAAATCTTCCAAGTATTGGAAGCCAAGAATACCATTGGATGTTGGCC 367 GTGACATGAAATCTTCATTTTCCAAGTATTGGAAGCCAAGAATACCATTGGATGTTGGCC TTGCTTCTTTAAGAAATGCTGCTAGTCATGGTGCAGCCTTTGTAGAATTTGACGTACACC 547 TITCAAAGGACTITGTGCCCGTGGTATATCATGATCTTACCTGTTGTTTTGACTATGAAAA AGAAATTTGATGCTGATCCAGTTGAATTTATTTGAAATTCCAGTAAAAGAATTAACATTTG AATCTGTGGTTCAGGAGGAAAATTCCTTTTCAGAAAATCAGCCATTTCCTTCTCTAAGA TGGTTTTAGAGTCTTTGCCAGAAGATGTAGGGTTTTAACATTGAAATAAAATGGATCTGCC **AGCAAAGGGATGGAATGGTAACTTATCAACATATTTTGACATGAATCTTTT** AGCAAAGGGATGGAATGTGGTAACTTATCAACATATTTGACATGAATCTGTTTT TGGATATATATTTAAAAACTGTTTTAGAAAATTCTGGGAAGAAGAGAGAATAGTGTTTTCTT CATTIGATGCAGATATTIGCACAATGGTTCGGCAAAAGCAGAACAAATATCCGATACTAT TTTTAACTCAAGGAAAATCTGAGATTTATCCTGAACTCATGGACCTCAGATCTCGGACAA **AAGACTTGCTCAGAAACCCATCCTATATTCAAGAGGCAAAAGCTAAGGGACTAGTCATAT** CCCCCATTGCAATGAGCTTTTGCACAGTTTTGAAAATCTACTGGGGATAAATGTACATACTG 1112 1292 607 1352 127 872 187 247 992 307 1052 1172 1232 1412 847 812 932 1472 1532 1592 1712 1027 727 787 907 1652 196 1772 1087 1832 ò - g ò g ò 엄 à qq ò 요 ò 셤 à q ò g g ò g g g a Š ò ò ò ð 엄 ò 임 g 셤 g 8 Š ò

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18-PEB-2003; 2003US-0448389P.
20-MAR-2003; 2003US-0466329P.
03-APR-2003; 2003US-0460279P.
13-MAY-2003; 2003US-0460279P.
13-MAY-2003; 2003US-04598106P.
14-SEP-2003; 2003US-0590179P.
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B-cell; Identifying a compound capable of treating a hematological disorder comprises combining a compound to be tested with a polypeptide related with the disorder under conditions suitable for binding of the test haematological; cytostatic; erythroid; anaemia; erythrocytosis; bone marrow; leukaemia; platelet; thrombocytopenia; thrombosis; T-cells; neutropenia; gene therapy; human; ss; gene; Narc16b. protein"

æ The invention relates to a novel method for identifying a compound capable of treating a haematological disorder which comprises combining compound to be tested with a specific polypeptide under conditions

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cc suitable for binding of the test compound to the polypeptide. The method CC of the invention has haematological and cytostatic applications and may be useful for identifying compounds for treating a haematological disorder associated with erythroid cells e.g. anaemia and erythrocytosis, come marrow e.g. leukaemia, platelets e.g. thrombocytopenia and thrombosis or B-cells and T-cells e.g. neutropenia. The compounds identified may be utilised during gene therapy procedures. The current cell center is that of a human haematological disorder-related cDNA of the convente con

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TCCCGGAAAACAATAGGCAAAGTGAGAGTTGACTATATAATTATTAAGCCATTACCAGGA 1044 204 264 120 324 180 384 240 444 300 504 360 564 420 624 480 684 540 744 600 804 9 864 720 924 780 984 840 9 GCGATATGTGGAAGCTGTGATGCTTTGGGAAACTGGAATCCTCAAAATGCTGTGGCTCTT CCTTTAGAAAGCGAAATTATTATTATTGACGATGGACAATTTGGAATCCACAATGGTTGAA CTGACACTAGAAGGCCTGGAGGAAGATGACGATGAGATAGGGTATCTCCCACTGTACTCCCAC ATGACACCTTCTCAGGTTGCCTTTGAAATAAGAGGAACTCTTTTACCAGGAGAAGTTTTT GCGATATGTGGAAGCTGTGATGCTTTGGGAAACTGGAATCCTCAAAATGCTGTGGCTCTT CTTCCAGAGAATGACACAGGTGAAAGCATGCTATGGAAAGCAACCATTGTACTCAGTAGA CTTCCAGAGAATGACACAGGTGAAAGCATGTATGGAAAGCAACCATTGTACTCAGTAGA GGAGTATCAGTTCAGTATCGCTACTTCAAAGGGTACTTTTTAGAACCAAAGACTATCGGT GGAGTATCAGTTCAGTATCGCTACTTCAAAGGGTACTTTTTAGAACCAAAGACTATTGGT GGTCCATGTCAAGTGATAGTTCACAAGTGGGAGACTCATCTACAACCACGATCAATAACC GGTCCATGTCAAGTGATAGTTCACAAGTGGGAGACTCATCTACAAAACCCACGATCAATAACC GAAAAAACCTCCTGTGTCAATAACCAAGAAAAAATTAAAAAATCTAGATTTAGGGTGAAG AAAATGTCCAATAGCTTGGAGATATCCTTAATAAGCGACAATGAGTTCAAGTGCAGGAT TCACAGCCGGAGTGTGTTATGGCTTGCAGCCTGATCGTTGGACAGAGTACAGCATACAG ACGATGGAACCAGATAACCTGGAACTAATCTTTGATTTTTTCGAAGAAGATCTCAGTGAG CACGTAGTTCAGGGTGATGCCCTTCCTGGACATGTGGGTACAGCTTGTCTTATCATCC CACGTAGTTCAGGGTGATGCCCTTCCTGGACATGTGGGGTACAGCTTGTCTTTATCATCC ACCATTGCTGAGAGTGCTGGAATTCTTACTCTTCCCATCATGAGCAGAAAT ACCATTGCTGAGAGTGGAAAGAGTGCTGGAATTCTTACTCTTCCCATCATGAGCAGAAAT ATGACACCTTCTCAGGTTGCCTTTGAAATAAGAGGAACTCTTTTACCAGGAGAAGTTTTT ACTCTGGATTCTGGATGGCTGACATGTCAGACTGAAATAAGATTACGTTTGCATTATTCT ACTOTIGGATICTIGGATIGGCTIGACATIGTCAGACTIGAAATAAGATTACGTTTTGCATTATTCT GAAAAACCTCCTGTGTCAATAACCAAGAAAAATTAAAAAAATCTAGATTTAGGGTGAAG CTGACACTAGAAGGCCTGGAGGAAGATGATGATAGGGTATCTCCCACTGTACTCCAC AAAATGTCCAATAGCTTGGAGATATCCTTAATAAGCGACAATGAGTTCAAGTGCAGGCAT Gaps ö CCTTTAGAAAGCGAAATTATTTGACGATGGACAATTTGGAATCCACAATGGT 13; Length 2019; BP; 633 A; 363 C; 449 G; 574 T; 0 U; 0 Other; Indels ö 8 Best Local Similarity 100.0%; Pred. No. 0; Matches 2019; Conservative 0; Mismatches Score 2019; 63.0%; Sequence 2019 745 145 205 265 121 325 385 241 445 301 505 361 685 541 601 805 865 925 985 Query Match 61 181 565 421 625 481 661 721 781

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02-MAY-2000; 2000JP-00183767.
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56.2%; Score 1803; DB 4; Length 1803;

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/product= "glycerophosphodiesterase 25"

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The present sequence encodes the human glycerophosphodiesterase 25 protein (I). (I) and the polynucleotide sequence encoding it (II) are applicable in the diagnosis and treatment of malignant tumnor. haemopathy, HIV infection, immunological diseases and various inflammation. (I) has cytostatic, anti-HIV, immunomodulatory and antiinflammatory activities. (I) is also useful for screening mimics, agonists, antagonists or inhibitors, or for use in peptide fingerprinting identification. The polynuclectide can be used as primers for nucleic acid amplification reaction or as probes for hybridisation reaction, or
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in producing gene chips or microarrays

Human glycerophosphodiesterase 25 and encoded polynucleotide, applicable in diagnosis and treatment of malignant tumor, hemopathy, HIV infection, immunological diseases and various inflammation.

Claim 6; Page 31-32; 37pp; Chinese

(BIOW-) BIOWINDOW GENE DEV INC SHANGHAI

WPI; 2001-418073/44. P-PSDB; AAB99775

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Sequence 1929 BP; 608 A; 298 C; 372 G; 651 T; 0 U; 0 Other;
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                              DB 4;
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Pred. No. 0;
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Matches 1711; Conservative
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Human; glycerophosphodiesterase 25; cytostatic; anti-HIV; tumour; immunomodulatory; antiinflammatory; haemopathy; HIV infection; immunological disease; inflammation; ss.

Location/Qualifiers 2. .694

sapiens

Homo

Human glycerophosphodiesterase 25 encoding cDNA SEQ ID NO:1.

(first entry)

21-SEP-2001

RESULT 13
AAH44173
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AAH44173;

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AAH44173 standard; cDNA; 1929

1679

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The present invention provides isolated nucleic acid molecules and proteins designated 27411, 23413, 22438, 23523, 25278, 26212, NARC SCI. NARC 10A, NARC 11, NARC 13, NARC 17, NARC 25, NARC 3, NARC 4, NARC 7, NARC 19, NARC 19, NARC 19, NARC 20, NARC 26, NARC 27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C,
TACACACTGTTGCTTTGTTGTTTTGTTGTGCGTGTGTTATACAGTAGTTAAATT
                                 TACACACTGTTGCTTTGTTGTTTTTTTTTTGTATGTGTGTTTATACAGTAGTTAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid molecules and polypeptides (e.g. 27411, 23
22438, 23553, NARC SC1 or NARC 1) useful for diagnosing, preventing
treating disorders associated with the protein, e.g. cancer,
                                                                                                                                                                                                                                            Neuronal apoptosis regulated candidate; NARC; diagnosis; cancer; lung disease; cirrhosis; hepatitis; atherosclerosis; myocardial infarction; inflammation; anaemia; glomerulonephritis; osteoporosis; AIDS; acquired immundeficiency syndrome; parkinson's disease; Alzheimer's disease; stroke; dermatitis; drug screening; gene therapy; cytostatic; hepatotropic; nootropic; cerebroprotective; dermatological; virucide; neuroprotective; phosphatidylglycerolphosphate synthase; POP synthase; rat; ss.
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Chiang LW, Hunter
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Kapeller-Libermann R, Meyers RE,
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22-OCT-1999; 99US-016118BP.
21-JAN-21990; 2000US-01495823.
28-FEB-2000; 2000US-01495523.
20-OCT-2000; 2000US-01495533.
31-JAN-2001; 2001US-00773426.
28-FEB-2001; 2001US-00773426.
31-OCT-2001; 2001US-0335037P.
25-MAR-2002; 2001US-00105992.
26-AUG-2002; 2002US-00129962.
30-OCT-2002; 2002US-00229662.
30-OCT-2002; 2002US-00284019.
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NARC 8B, NARC 9, NARC 2A, NARC 16B, NARC 1C, NARC 1A, NARC 25, 86604 or 13222. The invention is useful in diagnosing, preventing or treating disorders such as cancer, lung diseases, cirrhosis, hepatitis, atherosclerosis, myocardial infarction, inflammation, anaemia, glomerulonephritis, osteoporosis, AIDS (acquired immunedeficiency syndrome), Parkinson's disease, AIDS (acquired immunedeficiency dermatitis. These may also beed in drug screening. The invention is also useful in gene therapy. The present sequence is rat neuronal apoptosis regulated candidate (NARC) cDNA.
                                                                                                                                                                                          TAAGAGGAACTCTTTTACCAGGAGGCTCTTTGCATGTGTGGAACTGTGATGCCTTGG
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 86.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and proteins. These sequences can be used in the treatment of inflammatory conditions (eg arthritis, Crohm's disease), cancer, central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's and Huntington's diseases, spinal cord disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid cell disorders, platelet disorders, stem cell disorders, bone degenerative disorders, autoimmune disorders, for example multiple sclerosis, diabetes and arthritis, viral and bacterial infections, allergies and blood coagulation disorders. The present sequence is a DNA
                                                                                                                                                                                                                  wlnerary;
                                                                                                                                                                                                             Human; bone marrow; cytostatic; antirheumatic; antiarthritic; vulnerary; antiinflammatory; antibacterial; immunosuppressive; vasotropic; cancer; antiparkinsonian; neuroprotective; noctropic; haemostatic; osteopathic; antiulcer; fungicide; antidiabetic; antiasthmatic; antiallargic; immunostimulant; analgesic; cerebroprotective; antianaemic; infection; nervous system disorder; autoimmune disorder; inflammation; allergy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New bone marrow-expressed nucleic acids and polypeptides, useful for diagnosis, treatment of inflammatory, autoimmune, neurological, cancer and increasing hematopoiesis, stem cell survival and bone growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention relates to bone marrow expressed polynucleotides
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23-AUG-2000; 2000US-00649167.
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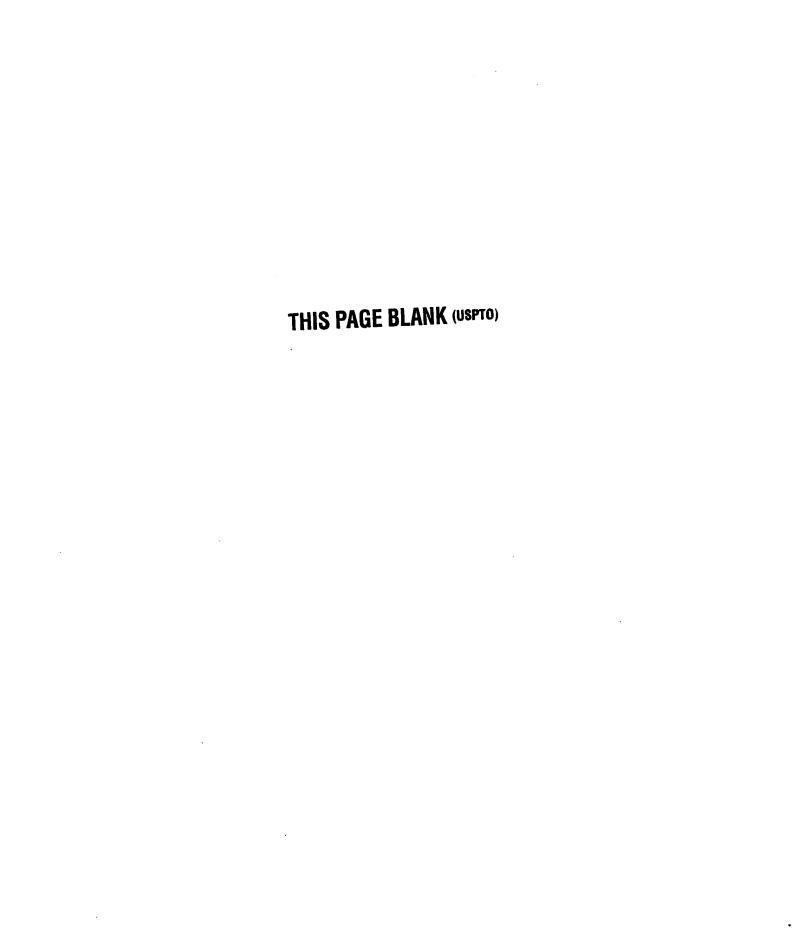
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FQVEQLERLKQELPELKNCLCPTVSHFIPSSFCVEPDIHVDANGIDSVENA"
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          Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

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                                                                                                                                   TGACACCTTCTCAGGTTGCCTTTGAAATAAGAGGAACTCTTTTACCAGGAGAAGTTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 GAGTATCAGTATCGCTACTTCAAAGGGTACTTTTTAGAACCAAAGACTATCGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCCATGTCAAGTGATAGTTCACAAGTGGGAGACTCATCTACAACCACGATCAATAACCC
                                                                                         Gaps
                                            81;
    Length 3142;
                                            Indels
Score 2038; DB 3;
Pred. No. 0;
0; Mismatches 450;
    63.6%;
82.9%;
                                                 Matches 2579; Conservative
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/sex="male"
| Call type="tumor"
| tissue type="tumor"
| clone lib="RIKEN full-length enriched mouse cDNA library"
| dev stage="adult"
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Institute, Department of Molecular and Cellular Biology, Elm and Carlton Streets, Buffalo, NY 14263, whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGACACTAGAAGGCCTGGAGGAAGAAGATGACGAT-----GATAGGGTATCTCCCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="hypothetical Glycerophosphoryl diester
phosphodiesterase/Glycosyl hydrolase, starch-binding
domain containing protein (InterPro|IPR004129,
InterPro|IPR002044, evidence: InterPro)
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0; Mismatches 450; Indels
                                               acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                   /db_xref="FANTOM_DB:C730037B04"
/db_xref="taxon:10090"
/clone="C730037B04"
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                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="putative"
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Best Local Similarity 82.9%;
Matches 2584; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Konno, H., Akiyama, J., Nishi, K., Kifeunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, A., Yoneda, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Pukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayateu, N., Hiramcto, K., Hiradoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kaukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Mateuyama, T., Miyazaki, A., Murata, M., Okazaki, Y., Saito, R., Saito, R., Saitoh, H., Sakai, R., Ohno, M., Ohaato, C., Sakai, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tagami, M., Tagawa, A., Shiraki, T., Takaku, T., Takaku, T., Takaku, T., Takaku, T., Takaku, T., Takaku, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A., Toya, T., Yasunishi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission

Direct Submission

Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse Lissues. Tissue was provided by William A. Held, Roswell Park Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases I to 3614)
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                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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       starch-binding domain containing protein, full insert sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection
                                                                                                                                                                                                                                      Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
9927923
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                                                       AK050318.1 GI:26093898
HTC; CAP trapper.
Mus musculus (house mouse)
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CTCAGATCTCGGACAACCCCCATTGCAATGAGCTTTGCACAGTTTGAAAATCTACTGGGG 	1816 ATMANICITGANGACTICCTCAGAMACCCATCCTATATTCAGGGGAAAGGT 1875	1936 TTGAAGGAACTTGGAGTTAATGGTCTAATTTATGATAGGATATATGATTGGTGCCTGAA 1995		2116 GATATCCAGTGCGATGCCAACGCGATTGATAACGTGGAAGATTTTATTGCAC 2175 2098 GATATCCACGTGGATGCCAACGCCATTGATAGTGCTGGAGAACGCTTAGTTCACGTGCAC 2157 2176 AGAGGTCATTTTGGGGGGGTGCACGCTGTTCGGGTATTTTTCATTCA	2236 TGTTGATCTATGCCTTTTGGGCTTCTCACTTCAATGAAGCAATAATGAAGTATTTAACTC 2295	2349 TGCCAGTCAGTCTTTATAGTCAGAAAATTTATTGGTTAGTAATATAAAATTTTTAAAC 2408 2330 TACCAATCAGTCTCTGTACAATAAGAAATATACTGTTAAACATTTCAGT 2379 2409 TAAATATAAAATCTATAAATGTTAAACATATGTCATTAAAAGCATTTGAATT 2468 [AACTATATAAATAGCTCGTATTTACACTTACAGCTTTTCATTTGATCAGGTCTGAAATCT	CARTICITION	2649 ATAGGTATTTTTACATGGGGTTCACCACACACACCATTTTATTCATTC	2660 TCAGATTGCTGCCATTTCTCACCTGACCCAAGCCTGCAGATGAACCTCAAAACTTG 2719 2769 TTCATAAATCTTTCAAAAGTTGTTTTACATGATGAAAATTTCAAAATGCTGCAGGG 2828
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598 CTCACACTCGAGGGTCTGGAGGAAGATGAAGATGATGATGACGATAAGGTCTCTCCCCACT 657 676 GTACTCCACAAAAATGTCCAATAGCTTGGAGATATCCTTAATAAGGGACAATGAGTTCAAG 735	TGCAGGCATTCACAGCCGGAGTGTGGTTATGGCTTGCAGCCTGATCGTTGGACAGAGTAC	778 AGCATACAGAACCAGATAATCTGGAGCTCATCTTTGACTTTTTGAGGAAGAT 837 856 CTCAGTGAGCACGTAGTTCAGGGTGATGCCCTTCCTGGACATGTGGGTACAGCTTGTCTC 915 838 CTCAGTGAGCATGTAGTTCAGGGTGATGTTCTTCCTGGACACGTGGGCACAGCTGCCTC 897	916 TTATCATCCACCATTGCTGGAAGGGGGGGGTGGGAATTCTTACTCTCCCATCATG 975	1036 TTACCAGGATACAGTIGIACATGAAATCTTCATTTTCCAAGTATTGGAAGCCAAGAATA 1095	GTTCAAGAAATACTATTGCTTCTTAAGAAATGCTGCTAGTCATGGTGGGGCGCCTTTGTA [AGCCA AGCCA AGCCA		1576 GACATGAATCTGTTTTTGGATAAATTTTAAAACTGTTTTAGAAATTCTGGGAAGAGG 1635 	1618 AGAATAGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

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/db xref="taxon:10090"
/clone="IMAGE:3596618"
/tissue type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal Carcinoma. S month old virgin mouse."
/clone lib="NCI CGAP_Mam6"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 16 Row: 1 Column: 21 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCCAGAGAATGACACAGGGTGAAAGCATGCTATGGAAAGCAACCATTGTACTCAGTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 TTAATGAAACGAGACAGGAGACAGTGTGTTGTGGAAAGCAGTGATTGCTCTCAATAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 GAGTATCAGTTCAGTATCGCTACTTCAAAGGGTACTTTTAGAACCAAAGACTATCGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u> aganaccicciciticantingcangananacticananantcangatitnaggenanangc</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 CGATATGTGGAAGCTGTGATGCTTTGGGAAACTGGAATCCTCAAAATGCTGTGGCTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               386 GICCATGICAAGIGAIAGIICACAAGIGGGAGACICATCIACAACCACGAICAAIAACCC
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                                                                  Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 58.7%;
Best Local Similarity 80.5%;
Matches 2508; Conservative
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                                                                        2766 TAACTTAATGTATAAAGTATTTGTAAG---AAGTATATTTTGCATATATAGTAGTGTAGA 2822
                                                                                                                                                                                    2823 ICAGAAGGIATCAATITGACICAATGCATGCTTTAAGGTTTTAAGCATGAGATTGTACATG 2882
                                                                                                                                                                                                                                                   TTTACTGTTAGGTCCTTGCATCTGTGGTGCTAGGTGAGTATGAGAAGATGTCAAGGACTG 3008
                                                                                                                                                                                                                                                                                                            2883 TTTACTGTTAAGTCCTTGCATC--TGGTGCTAGGTGAG-----GGAGATGTTAAGGACAT 2935
                                                                                                                                                                                                                                                                                                                                                                     3009 GACGIAITITGIIGCCIAAAAAAAAAGGCIGIIIGIAGGCGIIIIAAAIAIAIGCIIAIII 3068
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Mus musculus RIKEN CDNA 2310032D16 gene, mRNA (cDNA clone
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Submitted (27-APR-2001) National Institutes of Health, Mammalian
Submitted (27-APR-2001) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3053 GIGTIGCATAGTAGTIAAATITCCCATGCAGAAAATAAATGTCCTGAATITCTCAAA 3108
               TAATTTAATGTATAAAATTTAGTAAGAAAAGTATGTATTGCATACTTAGTAGAATAGA
                                                                                                                                    2889 TCACAACATACAAATTCAATTCAGTGCATGCTTTAGGTGTTAAGCATGAGATTGTACATG
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Email: cgapbs-r@mail.inh.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAGE:3596618), containing frame-shift errors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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AUTHORS
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KEYWORDS
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512 TCACACTCCACAGATCTCCACACACTCCACACATCACTCCCACTC 591	

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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,700 full-length CDNAs

L Nature 420, 563-573 (2002)

E (bases I to 3578)

S Adachi, J. Aizawa, K. Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Haragaki, T., Haraka, T., Hirozane, T., Hayashida, K., Hayateu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawat, J., Kojima, Y., Itoh, M., Kagawa, I., Kasukawa, T., Koya, S., Konno, H., Koda, M., Nowara, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Saito, R., Shibata, K., Shibata, K., Shibata, R., Shibata, R., Shibata, R., Shibata, R., Shibata, R., Takaku-Akahira, S., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-ULI-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, UKL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA library was prepared and sequenced in Mouse Genome Encyclopedala Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepare mouse tissues.
Please visit our web site for further details.
URL:http://gancome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FaNTOM DB:6030473012"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1794.6;
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205. .2109
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Direct Submission
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                   AATTTAATGTATAAATATTAGTAAGAAAAGTATGTATTGCATACTTAGTAGAATAGAT 2889
                                                           2700 AACTTAATGTATAAAGTATTTGTAAG---AAGTATATATTGCATATATAGTAGTGGTGGAT 2756
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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CTTCCAGAGAATGACACAGGTGAAAGCATGGTATGGAAAGCAACCATTGTACTCAGTAGA	386 GGAGIGICAGIGAAGIACCGCIACTICAGAGGCIGCTITITAGAACCAAAGACIAICGGI 445 385 GGTCCAIGICAAGTGAIAGITCACAAGIGGAGACTCAICIACAACACCACGAICAATAACC 444		ACTCTGGATTCTGGATGCCTGACATGTCAGACTGAAATAAGATTACGTTTGCATTATTCT	GAAAAACCTCCTGTGTCAATAACCAAGAAAATTAAAAAAATCTAGATTTAGGGTGAAG	CTGACACTAGAAGGCCTGGAGGAAGATGACGATGATAGGGTATCTCCCACTGTACTCCAC	AAAATGTCCAATAGCTTGGGGATATCCTTAATAAGCGACAATGAGTTCAAGTGCAGGAT 	745 TCACAGCCGGAGTGTGGTTATGGCTTGCAGCCTGATCGTTGGACAGAGTACAGCATACAG 804	805 ACGATGGAACCAGATAACCTGGAACTAATCTTTGATTTTTTCGAAGAAGATCTCAGTGAG 864 	865 CACGTAGTTCAGGGTGATGCCCTTCCTGGACATGTGGGTACAGCTTGTCTTATCATCC 924	925 ACCATTGCTGAGAGTGGGAAAGAGTGCTGGAATTCTTACTCTTCCCATCATGAGCAGAAAT 984	985 TCCCGGAAAACAATAGGCAAAGTGAGAGTTGACTATATAATTATTAAGCCATTACCAGGA 1044 	1045 TACAGTTGTGACATGAAATCTTCATTTTCCAAGTATTGGAAGCCAAGAATACCATTGGAT 1104 	TCAAGAA ACAGGAA	1165 AATACTATTGCTTCTTTAAGAAATGCTGCTAGTCATGGTGCAGCCTTTGTAGAATTTGAC 1224 1111 AATACTATCGCTTTTAAGAAATGCTGCCAGTCATGGCGCAGCATTTGTAGAAATTTGTA		ATGAAAAAGAAATTTGATGCTGATCCAGTTGAATTATTTGAAATTCCAGTAAAAGAATTA	1231 AIGAAGGAAATAIGAAGCIGAICCAGITGAATTGITGAAATTGITAAAATGCCAGIAAAAGAATTA 1290 . 1345 ACAITTGACCAACTCCAGITGITAAAGCTCACTCATGIGACTGCACTGAAATCTAAGGAT 1404

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Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Lof 60,770 full-length cDNAs

Lof 60,770 full-length cDNAs

Lof 60,877 full-length cDNAs

E (bases 1 to 2604)

Rachi, U., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninol, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Furuno, M., Hori, F., Inotani, K., Ishii, Y., Itoh, W., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasto, R., Sakai, C., Sakai, K., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Tagawa, A., Takahashi, F., Tanaka, T., Tajima, Y., Toya, T., Yamamura, T., Yasunishi, R., Yoshida, K., Yoshida, K., Shibata, W., Wuramatsu, M. and Hayashizaki, Y., Voshida, K., Shibata, M., Muramatsu, M. and Hayashizaki, Y., Yoshida, K., Shibata, M., Andawara, T., Yasunishi, A., Yoshida, K., Shibata, M., Muramatsu, M. and Hayashizaki, Y.
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                                                                              genes
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                                                                                                                                                                                                                         Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, M., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakguchi, S., Ikegami, T., Kashiwaqi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahixi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Maxazki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The FANTOM Consortium and the RIKEN Genome Exploration Research
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new GGenome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The RIKEN Genome Exploration Research Group Phase II Team and
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Nature 409, 685-690 (2001)
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/mol_type="mRNA"
/strain="CS7BL/6J"
/db_xref="FANTOM DB:2310032D16"
/db_xref="taxon:10090"
/clone="2310032D16"
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                      AAGCCTATAATGGTGA----ATCTTCATTAAAAG-----TTGGAAATTAACGATATA 2400
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                 2461 GAGAAAATGA--TTGCATAATTATACCTGACCATGGAAAAACTAAGTACCTC-AATGCA
                                                                                                                                                                                                                                                                                                                                        TGCATTTGCACTGGTGATTCCAACTGCACAAATCTTTGTGCCATCTTGTATATAGGTATT
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                                                                                    AATAGCTCATATTTACACTTACAGCTTTTCATTTGATCAGGTCTGAAATCTTTAGCACTT
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Pred. No. 0;
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/db_xref="G1:26365211"
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Group Phase I & II Team.

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

Analysis of the mouse transcriptome based on functional annotation

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Adachi, J. Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

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Sogabe, Y., Tagami, M., Tagawa, A., Toya, T., Yasunishi, A.,

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Fax:81-45-503-9216)

Fax:81-45-503-9216)
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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/dev_stage="12 days embryo"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Glycerophosphoryl diester phosphodiesterase/Glycosyl hydrolase, starch-binding domain containing protein (InterPro|IPR004129, InterPro|IPR002044, evidence:
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 81.9%;
Matches 1878; Conservative
                                               InterPro)
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/dev_stage="7 days embryo"
                                                                                                                                                                                                                                          Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
(bases 1 to 1618)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Research Group in Riken
                                                              RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                         FANTOM Consortium and the RIKEN Genome Exploration Research
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                                                                                                                      Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1618;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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                                    1823 TTCTCACCTGACCCCAGCCTGCAGATGAACCTCAAAACTTGTCTCATAAACCATC 1882
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched library, clone:C430017C03 product:hypothetical Glycerophosphoryl diester phosphodiesterase/Glycosyl hydrolase, starch-binding domain containing protein, full insert sequence.
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                                                                                                                                2784 AAAAGTTGTTTTACATCAATGTTAAAATTTTCAAAATGCTGCAGGGTAATTTAATGTATAA
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Meth. Enzymol. 303, 19-44 (1999)
99279253
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HTC; CAP trapper.
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39

07-APR-2004

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In (Mars. 100 1000).

Full-length cDNA libraries and normalization
In Unpublished (2001)
On May 1, 2003 this sequence version replaced gi:30311247.
On May 1, 2003 this sequence version replaced gi:30311247.
Contact: Genoscope
Contact: Genoscope - Centre National de Sequencage
Z rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqre@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a Noti-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTGCACTGAAATCTAAGGATCGGAAAGAATCTGTGGTTCAGGAGGAAAATTCCTTTTCA 1443
                                                                                                                                                                                             1006 bp mRNA linear EST 07-APR-2004 sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
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                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db xref="taxon:960"
/clone="CSODIO159YON"
/clone="CSODIO159YON"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tis strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                98 GCGTTTTAAATATGCTTATTTGTGTGTCTCTCACTACCTATTACACACTGTTGCTTTGT
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1. .1006
                                                                                                                                                                                                                                                                                                                                                              Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
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                                                                      GGGTTTGTTTTGTATGTGCGTGTGTTATACAGTAGTTA 3145
                                                                                      Score 921.4; DB 5;
Pred. No. 6.4e-203;
8; Mismatches 19;
                                                                                                                                                                                               BX344123 1006 bp mRNA 1005 bp mRNA 1005 bp mRNA 10344123 Homo sapiens PLACENTA COT 25-NORW Clone (SVDI059YA01 5-PRIME, mRNA sequence-BX344123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                        Mammalia, Eutheria, Primates;
1 (bases 1 to 1006)
                                                                                                                                                                                                                                                                   BX344123.2 GI:46264695
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97.0%;
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Homo sapiens
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/tismuc type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lib strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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0
                                                                                                                                                              Length 998;
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                                                                                                                                                              Score 962.6; DB 5;
Pred. No. 1.7e-212;
                                                                                                                                                                                               14; Mismatches 19;
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                                                                                                                                                              30.0%;
96.7%;
                                                                                                                                                                Query Match
Best Local Similarity 96.7%
Matches 965; Conservative
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/ organism="Homo sapiens"
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/ organism="Homo sapiens"
/ db xref="taxon:9606"
/ clone="IMAGE:5498838"
/ tissue type="lymphoma, cell line"
/ tasue type="lymphoma, cell line"
/ lab_host="DH108 [Apage-resistant)"
/ clone lib="NIH MGC 85"
/ note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
/ site_2: sall; Cloned unidirectionally; oligo-dT primed.
/ site_2: sall; Cloned unidirectionally; oligo-dT primed.
/ Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies.
/ Note: this is a NIH_MGC Library."
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DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov
http://mage.llnl.gov d column: 07
High quality sequence stop: 652.
Location/Qualifiers
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Homo sapiens cDNA clone IMAGE:5498838
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NIH-MC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Pration: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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BQ049943
AGENCOURT_7048600 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5787913
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I Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies (Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGENCOURT 6508010 NIH MGC_67 Homo sapiens cDNA clone IMAGE:55785025', mRNA Sequence.
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26.0%; Score 835; DB 4; Length 1128;
Best Local Similarity 91.6%; Pred. No. 7.8e-183;
Matches 1008; Conservative 0; Mismatches 71; Indels 2:
                                                                                                                                                                                                                                                                                                   CC-TTTTGGGCTTCTCAG-TTCAATGAAGCAATAA 2280
                                                                                                                                                                                                                                                                                                                                  BM478430.1 GI:18527472
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AUTHORS
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Directionally cloned using the following adaptors:
5'-TCGACCACGCCGTCGG-3' and sade by oligo-dT priming.
1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

B. (bases 1 to 948)

B. (bases 1 to 948)

NIH-WGC http://mgc.nci.nih.gov/.

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Llocation/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BU145581 948 bp mRNA linear EST 03-SEP-2002 AGENCOURT 8125917 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:6177333 5', mRNA sequence.
                                                                                                                                                                                                                                                                                541 TTGCCAGTCAGTCTCTTTATAGTGAGAAAATTTATTGGTTAGTAATATAAATATTTAAA
                                                                                                                                                                                              TAACTATATAAATAGCTCATATTTACACTTACAGCTTTTCATTTGATCAGGTCTGAAATC
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    .948
    /organism="Homo sapiens"

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                                                         1 (bases 1 to 973)

National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov,
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayaged by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NHH_MGC_85"
/note="Grgan: lymph, Vector: pCMV-SPORT6; Site 1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1:867 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NHH_MGC Library."
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                    Chordata, Craniata, Vertebrata, Eutele
Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 735. Location/Qualifiers 1, .973
                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
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                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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-	യഗ ച		AUTHORS Genoscope. TITLE Direct Submission JOURNAL Submitted (20-701-20	COMMENT 1st strand cDNA was enderogener of the control of the cont	was normalized. Libr division of Invitrog FEATURES division Location/Ou		/Lissue typ /plasmid="po	Ouery Match 25.2%; Best Local Similarity 99.9%; Matches 810; Conservative	Qy 2372 AGAAAATTTATTGGTTAG 	Qy 2432 AAACHTATGTTCATTAAA	Qy 2492 ACACTTACAGCTTTTCAT	Qy 2552 TGCATAATTATACCTGAC	Oy 2612 TGATTCCAACTGCACAAA	Qy 2672 ACATGCACACACAT 	Qy 2732 TTAACCAAACCAGCCTGA	Qy 2792 TTTACATCAATAAAA
<pre>Best Local Similarity 96.6%; Pred. No. 3e-178; Matches 887; Conservative 0; Mismatches 23; Indels 8; Gaps 5 1430 AAAATTCCTTTTCAGAAAATCAGCCATTTCCTTCTTTAAGATGGTTTTAGAGTCTTTGC 148 </pre>	QY 1490 CAGAAGATGTAGGGTTTAACATTGAAATAAAATGGATCTGCCAGCAAAGGGATGGAATGT 1549	Qy 1550 GGGATGGTAACCTATCAACATATTTTGACATGAATCTGTTTTTGGATATATTTTAAAAA 1609 	OY 1610 CTGTTTTAGAAAATTCTGGGAAGAGAGAATAGTGTTTTCTTCATTTGATGCAGATATTT 1669 181 CTGTTTTAGAAAATTCTGGGAAGAGAGAATAGTGTTTTCTTCATTTGATGAGAGAGA	OY 1670 GCACAATGGTTCGGCAAAAGCAGAACAATATCCGATACTTTTTAACTCCAAGGAAAAT 1729	OY 1730 CTGAGATTTATCCTGAACTCATGGACCTCAGATCTCGGACAACCCCCATTGCAATGAGCT 1789	OY 1790 TTGCACAGTTTGAAAATCTACTGGGGATAAATGTACATACTGAAGACTTGCTCAGAAACC 1849	OY 1850 CATCCTATATTCAGAGGGAAAGGTAAGGACTAGTCATATTCTGGTGGGGTGATGATA 1909	OY 1910 CCAATGATCCTGAAAACAGAAGGAAATTGAAGGAACTTGGAGTTAATGGTCTAATTTATG 1969	QY 1970 ATAGGATATATGATTGGATGCTGAACAACCAAATATATTCCAAGTGGAGCAATTGGAAC 2029	OY 2030 GCCTGAAGCAGAATIGCCAGAGCTITAAGAGCTGTTIGTGTCCCACTGTTAGCCGCTTTG 2089	QY 2090 TTCCTCATCTTTGTGTGGGGAGTCTGATATCCATGTGGATGCCAACGCATTGATAACG 2149	Qy 2150 TGGAGAATGCTTAGTTTTTATTGCACAGAGGTCATTTTGGGGGCGTGCACCG-CTGTTCT 2208 Db 721 TGGAGAATGCTTAGTTTTATTGCACAGAGGTCATTTTGGGGGCGTGCACCGCTGTTCT 780	Qy 2209 GGGTATTCATTATCACTGAGCATTGTTGATCTATGCCTTTTGGGCTTCTCAGT 2265	QY 2266 TCAATGAAGCAATAATGAAGTATTTAACT-CTTTCACTACAG-TTCTTGCAAGTATGC 2321	Oy 2322 TATTTAAATTACTTGGCC 2339 Db 901 TAATTAAATACTTTGGC 918	

CR623938 811 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DB002YJ01 of Neuroblastoma Cot 10-normalized of Homo sapiens (human).

RESULT 14 CR623938 LOCUS DEFINITION

Extract with a NotI-oligo(dT) primer. Five prime te-strand cDNA was digested with Not I and cloned EcoR V sites of the pCMVSPORT 6 vector. Library vary was constructed by Life Technologies, a 2431 2491 2611 ATCTTTGTGCCATCTTGTATATAGGTATTTTTTACATGGGTTG 2671 2731 2791 2851 TAAGAAAAAGTATGTATTGCATACTTAGTAGAATAGATCACAACATACAAATTCA 2911 ô 120 240 300 1004) Genoscope - Centre National de Sequencage : edex - FRANCE (E-mail : seqref@genoscope.cns.fr pe.cns.fr) BAAGGTGAACCTCGAAACTTGTTTCATAATCTTTCAAAAGTTG 420 9 Chordata, Craniata, Vertebrata, Euteleostomi, Primates, Catarrhini, Hominidae, Homo. AAGCATAGCACTTTGAAATTAACTATATAAATAAGCTCATATTT NTITICATICAGIAIGAACCIIGAGGCIGCIGCIGCAIITITICCAC GTAATATAAATATTTTAAACTAAATATATAAATCTATAATGTT AAGCATAGCACTTTGAAATTAACTATATAAATAGCTCATATTT CCATGAAAAAAAAAGTACCTCAAATGCATGCATTTGCACTGG BAGGTGAACCTCGAAACTTGTTTCATAAATCTTTCAAAAGTTG Gaps ig Email : fliang@lifetech.com URL :
.nvitrogen.com/ InVitroGen Corporation 1600 ; 0 rtaxon:9606" \$0DB002x701" pe="Weuroblastoma Cot 10-normalized" PCMVSPORT_6" 811; k; Score 809.4; DB 3; Length k; Pred. No. 6.6e-177; Indels Jessee, J. and Polayes, D. braries and normalization 1; 0; Mismatches "Homo sapiens" ogen. Qualifiers "mRNA" 4745 2852 421 3 A S

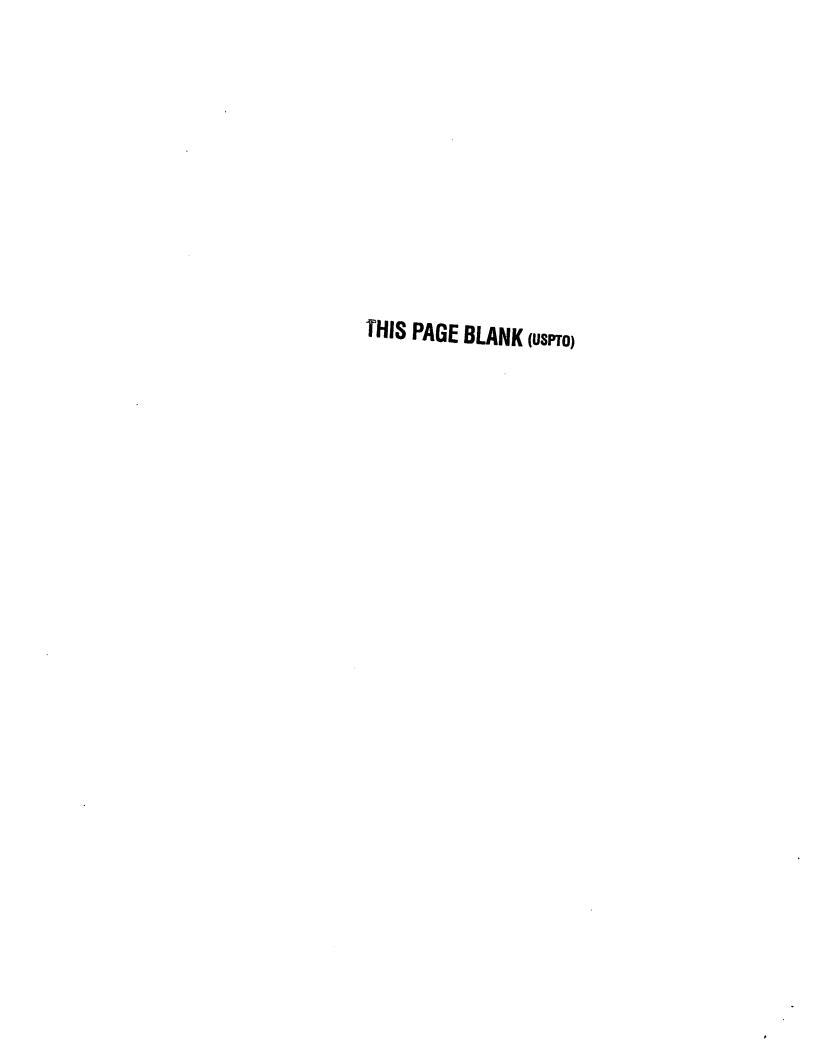
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Genoscope National de Sequencage Genoscope - Centre National de Sequencage Genoscope - Centre National de 5706 - 91057 EVRY cedex - FRANCE Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoX V sites of the pCMVSPQRT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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AL520917 Homo sapiens NEUROBLASTOMA COT 10-NORWALIZED Homo sapiens CDNA clone CSODB002YJ01 5-PRIME, mRNA sequence.
AL520917
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/clone lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Catarrhini; Hominidae; Homo.
                                                                                                                GTGGTGCTAGGTGAGTATGTATGAGGACGTGACGTATTTTGTTGCCTAAAAAA
TAAGAAAAAGTATGTATTGCATACTTAGTAGAATAGATCACAACATACAAATTCAATTCA
                              AAAAGGCTGTTTGTAGGCGTTTTAAATATGCTTATTTTGTGTGTCTCTCACTACCTATTA
                                                                                                                                                                               CACACTGTTGCTTTGTGGGTTTGTTTTGTATGTGCGTGTGTTATACAGTAGTTAAAATTTC
                                                                                               2972 GTGGTGCTAGGTGAGTATGAGAAGATGTCAAGGACTGGACGTATTTTGTTGCCTAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukary Organia, Metazoa, Chordata, Craniata, Vertebrata, Buteleo Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 811) [Liw.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001) [On Feb 13, 2001 this sequence version replaced gi:31039233.
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Pred. No. 1.1e-174;
4; Mismatches 6;
                                                                                                                                                                                                                                                                                              CATGCAGAAAATAAATGTCCTGAATTCTCA 3182
                                                                                                                                                                                                                                                                                                                              811
                                                                                                                                                                                                                                                                                                               CATGCAGAAAATAAATGTCCTGAATTTTCA
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AAACATATGTTCATTAAAAGCATAGCACTTTGAAATTAAACTATATAAATAGCTCATATTT
                                  61 AAACATATGTTCATTAAAAGCATAGCACTTTGAAATTAACTATATAAATAGCTCATATTT
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Search completed: July 2, 2005, 19:42:19 Job time : 9990 secs



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Database

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AK122510 Mus muscu
BD149663 Primer fo
AX869601 Sequence
AC023409 Homo sapi
AL807386 Mouse DNA
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AX197615 Sequence
AX208231 Sequence
AX208231 Sequence
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Nucleic acid molecules derived from rat brain and programmed death models

Patent: WO 0131007-A 4 03-MAY-2001;

Millennium Pharmaceuticals, Inc. (US)

Location/Qualifiers
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Sequence 4 from Patent W00131007
AX127528
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6 AX865601
10 AL807386
2 AC131004
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6 BD154638
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AX208343
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CQ459591
CQ474018
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CQ504016
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VERSION
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BC027588 Homo sapi
CQ41392 Sequence
AB037855 Homo sapi
CQ4971865 Sequence
CQ497765 Sequence
AL833069 Homo sapi
AX127525 Sequence
AX1833069 Homo sapi
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BD156897 Primer fo
AX877873 Sequence
AX013479 Homo sapi
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BV177434 sqnm94654
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                                GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                            4708233 seqs, 24227607955 residues
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C0413929
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GAAITGCCAGAGCTTAAGAGCTGTTTGTGTCCCACTGTTAGCCGCTTTGTTCCTCATCT GATTGGATGCCTGAACAACCAAATATATTCCAAGTGGAGCAATTGGAACGCCTGAAGCAG

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     Millennium Pharmaceuticals, Inc. (US)
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2401 TITTAAACTAAATATATAAATCTATAATGTTAAAACATATGTTCATTAAAAGCATAGCACT
                                                                                            2461 TIGABATTAACTATATAAATAGCTCATATTTACACTTACAGCTTTTCATTTGATCAGGTC
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Narc10 and narc16, programmed cell death-associated molecules
uses thereof
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; B
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Sequence 4 from Patent WO02081516.
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AX675186.1 GI:29333417
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 34 Row: a Column: 18 This clone was selected for full.length sequencing because it passed the following selection criteria: matched mRNA gi: 25901061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MTPSQVAFEIRGTLLPGEVFAICGSCDALGNWNPQNAVALLPEN
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ESEIIIDDGQFGIHNGVETLDSGWLTCQTEIRLRLHYSEKPPVSITKKKLKKSRFRVK
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IQTMEPDNLELIFDPFEEDLSEHVVQCDALPGHVGTACLLSSTIAESGKSAGILTLPI
MSRNSRKTIGKVRVDYIIIKPLPGYSCDMKSSFSKYWKPRIPLDVGHRGAGNSTTTAQ
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DVGFNIEIKWICQQRDGMWDGNLSTYFDMNLFLDIILKTVLENSGKRRIVFSSFDADI
CTMVRQKQNKYPILFLTQGKSEIYPELMDLRSRTTPIAMSFAQFENLLGINVHTEDLL
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                                                                         Shiraki
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                                                                                                                                                                                                     contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 GGGCGGCGCGCGCGACGCGGACCTGCGGACTAGCGAACCCGGAGCACGACATAAA
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                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) &
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
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/protein_id="AAH27588.1"
/db_xref="GI:20379526"
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/db_xref="LocusID:56261"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:26147 IMAGE:4827346"
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ive 0; Mismatches
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clone_lib="NIH_MGC_97"
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wans, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morkernan, K.J., Mallahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalka, U., Smailus, D.E.,
Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.
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                                                                                                    AGAATAGATCACAACATACAATTCAATTCAGTGCATGCTTTAGGTGTTAAGCATGAGAT
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NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 25, 2003 this sequence version replaced gi:20379525.
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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1939 GASTAMAGNATINACATTCACCAMCTCATOTTOMAGCTCACTACTACTACACACTACTACACACTACTACACACTACT
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11 ITTOTACTORAGOCACTOTACTOCACTOCANGCOCACTOCACCACACTOCACACACACACACACACACACAC

6 8 6 8 6 8 6 8 6 8 6 8 6 8 6

/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Query Match 98.8%; Score 3166; DB 6; Length 3499; Best Local Similarity 99.8%; Pred. No. 0; Matches 3169; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	QY 11 GCGTCCGGGCGAGGAGCGCGGCGCCCGGTACCTCTGCCCGCGGTCCTCG 70	Qy 71 GGGGGGGGGGGGGGGGGGGGCGGGCTAGGGAACCCGGAGCACGACATCATAAA 130 Db 147 GGGGGGGGGGGGGGGGGGGGGACTGCGGACTAGCGAACCCGGAGCACATCATAAA 206	QY 131 ATANATCCATCAGAATGACACCTTCTCAGGTTGCCTTTGAAATAAGAGGAACTCTTTTAC 190	OY 191 CAGGAGAAGTTTTTGCGATATGTGGAAGCTGTGATGCTTTGGGAAACTGGAATCCTCAAA 250	OY 251 ATGCTGTGGCTCTTCCAGAGAATGACACAGGTGAAAGCATGCTATGGAAAGCAACCA 310	QY 311 TIGIRCICAGIAGAGATATCAGITCAGIACGIACTITTAGAAC 370 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 371 CAAAGACTATCGGTGGTCCATGTCAAGTGATAGTTCACAAGTGGGAAGACTCATCTACAAC 430 Db 447 CAAAGACTATCGGTGGTCCATGTCAAGTGATAGTTCACAAGTGGGAGACTCATCTACAAC 506	OY 431 CACGATCAATAACCCCTTTAGAAAGCGAAATTATTAGACGATGGACAATTTGGAATCC 490	Oy 491 ACAATGGTGTTGAAACTCTGGATTCTGGTTGACTGACATGTCAGACTGAAATAAGATTAC 550	QY 551 GTTTGCATTATTCTGAAAAACCTCCTGTGTCAATAACCAAGAAAAAATTAAAAAATCTA 610	QY 611 GATITAGGGTGAACTGACACTAGAAGGCCTGGAGGAAGATGACGATGATAGTC 670 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 671 CCACTGTACTCCACAAATGTCCAATAGCTTGGAGATATCCTTAATAAGCGACAATGGT 730	OY 791 AGTACAGCATGACGATGGAACCAGATAACCTGGAACTAATCTTTGATTTTTCGAAG 850	Qy 851 AAGATCTCAGTGAGCACGTAGTTCAGGGTGATGCCCTTCCTGGACATGTGGGTACAGCTT 910 1	911 GICTCTTATCATCCACCATTCCTGAGAGAGAGAGAGTGCTGGAATTCTTACTCTTCCCA 97	Db 987 GTCTCTTATCATCCACCATTGCTGAGAGTGGAAAGAGTGCTGGAATTCTTACTCCCA 1046
Qy 2471 CTATATAAATAGCTCATATTTACACTTTACAGCTTTTGATTGA	Qy 2531 AGCACTTAAGGAAAATGACTATGCATAATTATACCTGACCATGAAAAAAAA	Qy 2591 AAATGCATGCATTGCACTGGTGATTCCAACTGCACAAATCTTTGTGCCATCTTGTATAT 2650	Qy 2651 AGGIATTTTTACATGGGTTGACATGCACACACCACTTTTCATTCA	OY 2711 AGGCTGCTGCCATTTTTCCACTTAACCAACCTGAAGGTGAACCTCGAAACTTGTT 2770	Qy 2771 TCATAAATCTTTCAAAAGTTGTTTTACATCAATGTTAAAATTTCAAAATGCTGCAGGGTA 2830 	Qy 2831 ATTTAATGTATAAAATATTAGTAAGAAAAGTATGTATTGCATACTTAGTAGAATAGATC 2890 	Qy 2891 ACAACATACAAATTCAATTCAGTGCATGCTTTAGGTGTTAAGCATGAGATTGTACATGTT 2950	QY 2951 TACTGTTAGGTCCTTGCATCTGTGGTGCTAGGTGAGTATGAGAAGATGTCAAGGACTGGA 3010	QY 3011 CGTATITIGITGCCTAAAAAAAAGGCTGTTTGTAGGGGTTTTAAATATGCTTATTTTG 3070	OY 3071 TGTGTCTCTCACTATTACACACTGTTGCTTTGTGGGTTTGTTT	Qy 3131 GTTATACAGTAGTTAAATTTCCATGCAGAAAATAAATGTCCTGAATTCTCAAAAAAA 3190 	Qy 3191 AAAAAA 3196 Db 3259 AAAAAA 3264	RESULT 4 CQ413929 CQ413929 LOCAL LOCAL LOCAL DEFINITION Sequence 21000 from Patent WO0170979. ACCESSION CQ413929 CQ413929 CQ413929 GI:41321710	Homo sapiens (human) SM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;	Mammalla; Eutherla; Frimates; Catarrhin; Hominidae; Homo. REFERENCE 1 AUTHORS Lee,J. and Lillie,J. TITTE Genes. Compositions. kits. and method for identification.	assessment, prevention, and Patent: WO 0170979-A 21000 Millennium Pharmaceuticals.	FEATURES Location/Qualifiers source 13499

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1211 TIGTAGAATTIGACGTACACCTTICAAAGGACTTIGIGCCCGGTGGTATAICAIGAICTTA 1270
TTGTACTCAGTAGAGGAGTATCAGTTCAGTATCGCTACTTCAAAGGGTACTTTTAGAAC
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Nagase, T., Kikuno, K., Ishikawa, K.I., Hirosawa, M. and Ohara, O.
Prediction of the coding sequences of unidentified human genes.
XVI. The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro
DNA Res. 7 (1), 65-73 (2000)
                                                                           PRI 14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                              Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdhainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens mRNA for KIAA1434 protein,
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0; Mismatches
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/organism="Homo sapiens"
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/clone_lib="pBluescriptII
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Ohara,O., Nagase,T. and Kikuno,R.
Direct Submission
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/gene="KIAA1434"</pre>
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Pred. No. 0;
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 99.8%;
Matches 3168; Conservative
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 2731; Conservative 0; Mismatches
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Homo sapiens mRNA; cDNA DKFZp45101715 (from clone DKFZp45101715).
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1 (bases 1 to 6671)

Bloecker, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.

Direct Submission

Submitted (13-MY-2003) MIPS, Ingolstaedter Landstr.1, D-85764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKEZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.
Barunschweig/Germany) within the cDNA sequencing consortium of th
German Genome Project.
This clone (DKFZp45101715) is available at the RZPD in Berlin.
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/clone_lib="451 (synonym: hlcc1). Vector pSport1; host
DH10B; Sites NotI + SalI"
/dev_stage="adult"
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/mol_type="mRNA"
/db_txref="REXPD:DKFZp45101715"
/db_txref="laxon:9606"
/clone="DKFZp45101715"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Nucleic acid molecules derived from rat brain and jeath models
death models
Patent: WO 0131007-A 1 03-MAY-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX127525.1 GI:14134230
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Best Local Similarity 99.7
Matches 2486; Conservative
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                                                                                                                                                                                                                                                                                                                   Length 39694;
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Pred. No. 0;
0; Mismatches 141; Indels 419;
3 39694: contig of 22772 bp in length.
Location/Qualifiers
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                                                                                                                /chromosome="7"
/clone="XXFOS-87042610"
1. 7028
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7129. 16822
/note="assembly_name:Contig5"
                                                                                                                                                                                                                                       /organism="Homo sapiens'
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Best Local Similarity 84.2%;
Matches 2993; Conservative 0
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Homo sapiens chromosome 7 clone XXFOS-87042G10, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-APR-2003) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
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1 (bases 1 to 39694)
Waterston, R.H.
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                      GTGCATGCTTTAGGTGTTAAGCATGAGATTGTACATGTTTACTGTTAGGTCCTTGCATCT
                                                                                                                                                                              2347 AAAAGGCTGTTTGTAGGCGTTTTAAATATGCTTATTTTTGTGTGTCTCTCACTACCTATTA
                                                                                                                                                                                                                     CACACTGTTGCTTTGTTTGTTTTGTATGTGCGTGTGTTATACAGTAGTTAAATTTC
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Sequencing vector: plasmid; 100$
Sequencing vector: plasmid; 100$
Chemistry: Dye-primer ET; 0$ of reads
Chemistry: Dye-terminator Big Dye; 100$ of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 39167 bases at least Q40
Consensus quality: 39319 bases at least Q20
Consensus quality: 39366 bases at least Q20
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HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
HOmo sapiens (human)
Homo sapiens
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Unpublished
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Waterston, R.H.
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7129
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VERSION
KEYWORDS
SOURCE
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AC144439
LOCUS
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32438

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16;

Gaps

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32795

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431

32975

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731

32915

			1972 AGGATATATGATTGGATGCCTGAACCAAATATTTCCAAGTGGAGCAATTGGAACGC 2031 34645 AGGATATATGATTGGATGCCTGAACAACCAAGTGGAGCAATTGGAACGC 2031 34645 AGGATATGGATGCCTGAACAACCAAGTGGAGCAACTGGAATGC 2032 CTGAAGCAAGTTGCCAGGCTTAAGACTGTTGTGTCCCACTGTTAGCGCTTTGTT 2091 34694 CTGAAGCAAGAATTGCCAGAGTGTAAGGGCTGTTGTTCCCACTGTTAGCCACTTTGTT 34753 2092 CCCTCAATTTGTGGGGGAGTCTGATATCCATGTGGTCCCACTGTTAGCCACTTTGTT 34753 2092 CCCTCAATTTGTGGGGGAGTCTGATATCCATGTGGATGCCAACGCATTGATAAACGTG 2151		AACAATAATGAAGTATTTAACTCTTTCACTATAGTTCTTGCAAGTATGCTATTTAAATT AAACAATAATGAAGTATTTAACTCTTTCACTATAGTTGCAAGTATGCTATTTAAATT ACTTGGCCAGGTATAATTGCCAGTCAGTCTCTTTATAGTGAAAATTTATTGGTTAGTA ACTTAGCCAGGTGTAATTGCCAGTCAGTCTCTTTACAGTGAGAAATTGGTTAAAAG ATATAAAATTTTAAACTAAATTATAAATCTATAAATGTTAAAAG ATATAAAATTTTAAACTAAATATAAATCTATAATGTTAAAACATATGTTCATTAAAAG ATATAAAATATTTAAACTAAATATAAATCTATAAATGTTTAAATGTTCATTAAAAG	2452 CAIAGCACTTTGAAATTAACTATATAAATAGCCCATATTTACACTTACAGCTTTTCATT 2511 35110 CAIAGCACTTTGAAATTAAATAATAAATAGCACCATATTACACTTACAGCTTTTCATT 2511 2512 GATCAGGTCTGAAATTAAATATAAATAGGAAATGCTCATAATTATACCTGACCA 2571 2512 GATCAGGTCTGAAATCTTTAAGGAAATGACTAAGCATAATTATACCTGACCA 2571 35169 GATCAGGTCTGAAATCTTTAAGGAAATGACTATAGGTAATTATACCTGACCA 35228 2572 TGAAAAAAATAAGTACTCTAAAGGAAATGACTAGGGTAATTATACCTGACCAAATC 2631 35229 TGGAAAAAATAAGTACTCAAATGCATTGCACTGGTAATTTATACCTGACAAATC 2631 35229 TGGAAAAAAATAAGTACTCAAATGCATTGCACTGGTGATTCCAACTGCACAAATC 35288
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	B52 AGAICTCAGTGAGCACGTAGTTCAGGGTGATGCCTTCCTGGACATGTGGGTACAGCTTG 911		33512 TAAAGAAATACTATTGCTTCTTTAAGAATGCTGCTAGTCACGGTGCATACTTTTACGAATGCTGCTAGTCACGGTGCACGTTTTTACGATCTTACTACTACTACTACTACTACTTTCACGTACACTTTCACGTCCCGTGGTATATCATGATCTTAC 1271 33566 TGTAGAATTTGATGACCTTTCAAAGGACTTTGTGCCCCATGGTTATATTGAAATTCC 33625 1272 CTGTTGTTTGACTAAAAAAAAAAAAATTTGATGCTCAGTTGAATTATTTGAAATTCC 1331 33626 CTGTTGTTTGACTATGAAAAGAAATTTGATGCTGATCCAGTTGAATTATTTGAAATTCC 33685		1511 TTGAAATAGAATCTGCCAAAGGGATGGAATGTGGGATGGTAACTTATCAACAT 1570	33986 AGA-GAGAATAGTGTTTTTTTTTTTTTTTTTTTTTTTTT

Washington Missouri 63108, USA

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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see map position of this sequence, see map position of this sequence, see map position of this sequence, see mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted (20-APR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA (bases 1 to 149259)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (08-OCT-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA ON Apr 13, 2002 this sequence version replaced gi:19774659.
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 149259)
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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                                                                                                                                                                                             University, 4444 Forest Park Avenue, St. Louis, 6 (bases 1 to 149259)
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Contact: sapiens@watson.wustl.edu
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/db_xref="taxon:9606"
/chromosome="7"
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Submitted (03-APR-2002)
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Waterston, R.
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                                                                                                         Waterston, R.
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                                                                                                         5289 TTTGFGCCTTCTTGTATATAGGTATTTTTACATGGGTTGACATGCACATAACAGCATTT 35348
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens BAC clone RP11-1217F2 from 7, complete sequence.
AC099654
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Dignan,G., Kozlowicz,A. and Swearengen-Shahid,S.
The sequence of Homo sapiens BAC clone RP11-1217F2
Unpublished (2001)
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Genome Res. 8 (11), 1097-1108 (1998)
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Sulston, J.E. and Wilson, R.
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Waterston, R.H.
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4 (bases 1 to 149259)
Waterston, R.H.
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COMMENT Center: Washington University Genome Sequencing Center Center code: WUGSC Web site:http://genome.wustl.edu Contact: submissions@watson.wustl.edu Contact: submissions@watson.wustl.edu	* NOTE: This is a 'working draft' sequence. It currently * consists of 7 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gasps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved. * 1 8714: contig of 8714 bp in length	814: gon of 35261: contig 35261: contig 62200: contig 62300: gop of 114137: contig 114237: gap of 158156: contig 158256: gon of	* 15827 15928 Cohtig of 1372 bp in length * 15829 159728 Gopt of unknown length * 159729 160762 Contig of 1034 bp in length. FEATURES Location/Qualifiers 1 . 160762 Contig of 1034 bp in length. FEATURES 1 . 160762 Contig of 1034 bp in length. 	c_feature c_feature c_feature c_feature c_feature c_feature	, ; ; I DECE
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 1803)

RS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,

RS Ota,T., Isogai,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

Primer for synthesizing full-length cDNA and use thereof

Primer for Synthesizing full-length cDNA and use thereof

HELIX RESEARCH INSTITUTE

OS Homo sapiens (human)

PN JP 2002191363-A111740

PD 09-JUL-2002

PP 28-JUL-2000

PI 78-JUL-2000

PI 78-JUL-2000

PI SAITO,

PI SAITO,

PI SAITO,

PI KEIICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,

PI KEIICHI NAGAI, TETSUJI OTSUKI
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Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Sequence 39,

Sequence:

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; Sequence 4, Application US/10047855
; Publication No. US20030165863A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Lillian Wei-Wing
; TITLE OF INVENTION: NARC10 and NARC16, Programmed Cell
; TITLE OF INVENTION: Death-Associated Molecules and Uses Thereof
; FILE REPRENCE: 35800/242056
; CURRENT APPLICATION NUMBER: US/10/047,855
; CURRENT FILING DATE: 2002-01-15
; PRIOR PAPLICATION NUMBER: US 60/262,306
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
1 US-10-772-636-25

7 US-10-426-776-39

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7 US-10-005-4214

7 US-10-016-82-4214

9 US-10-015-81-11

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US-10-085-783A-35647
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100.0%; Pred. No. 0;
ive 0; Mismatches
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NAME/KEY: CDS
LOCATION: (145)...(2163)
NAME/KEY: misc_feature
LOCATION: (1)...(17)
COTHER INFORMATION: Vector sequence
US-10-047-855-4
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Best Local Similarity 100.
Matches 3206; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                    (without alignments)
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/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
                   GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-426-776-34
US-10-887-553A-1007
US-09-814-353-21000
US-10-357-930-2932
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Maximum DB
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DB 16; Length 3206;

Result No.

Sequence 71, Appl Sequence 71, Appl Sequence 199, Ap Sequence 1969, A Sequence 8067, Ap Sequence 8067, Ap Sequence 8067, Ap Sequence 183, App Sequence 183, App Sequence 1988, A Sequence 15054, A Sequence 2389, Ap Sequence 2389, Ap Sequence 2389, Ap Sequence 2389, Ap Sequence 2389, Ap Sequence 15054, A Sequence 15054,

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GENERAL INVORMATION:
APPLICANT: Gluckenan, Maria Alexandra
APPLICANT: Gluckenan, Maria Alexandra
APPLICANT: Gluckenan, Mark J.
APPLICANT: Raidolph-Carry Ying
APPLICANT: Raidolph-Carry Liberman, Rosana
APPLICANT: Raidolph-Carry Liberman, Rosana
APPLICANT: Madolph-Carry Liberman, Rosana
APPLICANT: Mayers, Raidolph-Carry
APPLICANT: Chiang, Lillian West-Ming
APPLICANT: Chiang, Lillian West-Ming
APPLICANT: Chiang, Lillian West-Ming
APPLICANT: Chiang, Lillian West-Ming
APPLICANT: Chiang, Lillian West-Ming
APPLICANT: WOOS, Andrew
APPLICANT: WOOS, Andrew
APPLICANT: WARC J., NARC 35, NARC 15, NARC 11, NARC 11,
TITLE OF INVENTION: NARC 144, NARC 15, NARC 15, NARC 16, NARC 17,
TITLE OF INVENTION: ANAC 144, NARC 15, NARC 19, NARC 26, NARC
TITLE OF INVENTION: ANAC 144, NARC 14, NARC 15, NARC 16, NARC 18, NARC 14,
TITLE OF INVENTION: Befold AND 3222 WOLECULES AND USES THEREFOR
TITLE OF INVENTION: Befold AND 3222 WOLECULES AND USES THEREFOR
TITLE OF INVENTION: Befold AND 3222 WOLECULES AND USES THEREFOR
TITLE OF INVENTION: Befold AND 3222 WOLECULES AND USES THEREFOR
TITLE OF INVENTION: WORBER: 09/1926 621
FRICK FILLING DATE: 2000-06-89
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100.0%; Pred. No. 0;
ive 0; Mismatches
Sequence 34, Application US/10426776
Publication No. US20040009553A1
GENERAL INFORMATION:
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Matches 3206; Conservative
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CORGANISM: Homo Sapiens
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971 TCATGAGCAGAAATTCCCGGAAAACAATAGGCAAAGTGAGAGTTGACTATATAATTATTA 1030
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Pred. No. 0;
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                                          Query Match
Best Local Similarity 99.8
Matches 3181; Conservative
; TYPE: DNA
; ORGANISM: human
US-10-887-553A-1007
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; Sequence 1007, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; APPLICANT: Garza, Dan
; TITLE OF INVENTION: With insulin signalling dysregulation
; TITLE OF INVENTION: With insulin signalling dysregulation
; FILE REFERENCE: 4-3362
; CURRENT APPLICATION NUMBER: US/10/887,553A
; CURRENT FILING DATE: 2004-07-08
; PRIOR PILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 1007
; LENGTH: 3265
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TITLE OF INVENTION: DOUGL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: DENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: DENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-066B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PSECSEQ for Windows Version 4.0
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; LOCATION: 3490, 3491, 3492, 3493, 3494, 3495, 3496, 3497, 3498, 3499
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-21000
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 3169; Conservative 0; Mismatches
                                                                                        RESULT 4
US-09-814.353-21000
S. Sequence 21000, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
                                                                                                                                                                                   Pamela
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ORGANISM: Homo sapiens
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AGCCATTCCTTCTCTAAAGATGTTTTAGAGTCTTTGCCAGAAGATGTAGGGTTTAACA TTGAAATAAAATGGATCTGCCAGCAAAGGGATGGAATGTGGGATGTTATCAACATTGAATAAAATGAAATGGATCTGCCAGCAAAGGGATGGAATGTGGGATGTAACTTATCAACATTTTGAATAAAATGAAATGGATCTTTTTGCCAGCAAGGGATGGAATGTTGTTTTAGAAATTTTTAGAAAATTTTTGACATGATTTTTGGATATAAAATTTTAAAAACTGTTTTTAGAAAATTCTGGGAATGTTTTTGACATGTTTTTGGATATAAAATTTTTAAAAACTGTTTTTAGAAAATTCTGGGAATGTTTTTGAAAAACTGTTTTTAGAAAATTCTTGGATAAAAAACTGTTTTTAGAAAATTCTTGGATATAAAAACTGTTTTTAGAAAATTCTTGGATATAAAAACTGTTTTTAGAAAAATTCTTGGATATAAAAACTGTTTTTAGAAAAATTCTTGATGTTTTTAAAAACTGTTTTTAGAAAAATTCTTGATGAAAAAGCTATTTTGAAAAACTGTTTTTAGAAAAATTTTGAAAAAACTGTTTTTAGAAAAATTTTGAAAAAACTGTTTTTAGAAAAATTTTTGAAAAAATTTTGAAAAAAATTTTGAAAAAA	1001 AGAGGAGAATAGTGTTTTCTTCATTTGAGGAGATATTTGCACAATGCTTCGGCAAAAGC 1766 1691 AGAACAAATATCCGATACTATTTTAACTCAAGGAAAATCTGAGATTTATCCTGAACTCA 1750	1897 IGGGGATAAATGTACATGAAGACTCAGAAACCCATCATATTCAAGAGGCAA 1946 1871 AAGCTAAGGACTAGTCATATTCTGCTGGGGGGTGATACCAATGATCAGAAACCAA 1930 1947 AAGCTAAGGGACTAGTCATATTCTGCTGGGGGGTGATGATACCAATGATCCTGAAAACAGAA 1930 1947 AAGCTAAGGGACTTATTCTGCTGGGGGGTGATGATACCAATGATCCTGAAAACAGAA 2006 1931 GGAAATTGAAGGAACTTGGGGTTAATGGTCTAATTTATGATGGATTATTGATTG	1991 CTGAACAAATATATTCCAAGTGGAGCAATTGGAAGCCCTGAAGCAGGAATTGCCAG 2050 2067 CTGAACAACCAAATATTCCAAGTGGAGCAATTGGAACGCCTGAAGCAGGAATTGCCAG 2050 2051 AGCTTAAGAGCTGTTTGTGCCCACTGTTAGCCGCTTTGTTCCCTCATCTTTGTGTGGGG 2110 2051 AGCTTAAGAGCTGTTTGTGCCACTGTTAGCCGCTTTGTTCCTCATCTTTGTGTGGGG 2110 2127 AGCTTAAGAGCTGTTTGTGCCCACTGTTAGCCGCTTTGTTCCCTCATCTTTGTGTGGGG 2110		
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                                             3498, 3499
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0
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; LENGTH: 3499
; TYPE: DNA
; CRGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3490, 3491, 3492, 3493, 3494, 3495, 3496, 3497,
; OTHER INFORMATION: n = A,T,C or G
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                                                                            Score 3164.4;
Pred. No. 0;
0; Mismatches
                                                                            98.7%;
                                                                            Query Match
Best Local Similarity 99.8
Matches 3168; Conservative
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GREREAL INFORMATION:

APPLICANT: Schlegel. Robert
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: HUMAN PROSIATE CANCER
TITLE OF INVENTION: HUMAN PROSIATE CANCER
FILE REFERENCE: MRI-OUTBCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR FILING DATE: 2000-02-16
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-06-09
PRIOR PRIOR APPLICATION NUMBER: 60/189,862
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR APPLICATION NUMBER: 60/199,007
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
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PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR PRILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29632
LEBORTH: 3499
TURNEY DATE
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                      NAME/KEY: misc feature
LOCATION: 3490, 3491, 3492, 3493, 3494, 3495, 3496, 3497, 3498, 3499
OTHER INFORMATION: n = A,T,C or G
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99.8%; Pred. No. 0;
tive 0; Mismatches
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Sequence 29632, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
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Matches 3168; Conserv
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Pred. No. 0;
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/185,517
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 10/105,992
PRIOR APPLICATION NUMBER: 09/406,045
PRIOR FILING DATE: 1999-00-27
PRIOR FILING DATE: 1999-00-27
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PRIOR FILING DATE: 2001-01-31
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PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 09/692,785
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Best Local Similarity 99.7%;
Matches 2486; Conservative
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US-10-426-776-32
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Sequence 22, Application US/10426776

Publication No. US20040009553A1

GENERAL INFORMATION:
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APPLICANT: Mayers, Rachel E.
APPLICANT: Hunter, John Joseph
APPLICANT: Hunter, John Joseph
APPLICANT: Honter, John Joseph
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APPLICANT: Honter, John Joseph
APPLICANT: Honter, John Joseph
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APPLICANT: Mayers, Rachel E.
APPLICANT: Mayer Sezis, Rachel E.
APPLICANT: Mayer Sezis, Rachel E.
APPLICANT: Honter, John Joseph
APPLICANT: Honter, John Joseph
APPLICANT: Warc 10, NARC 12, NARC 10, NARC 11,
TITLE OF INVENTION: NARC114, NARC 15, NARC 16, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10, NARC 10,
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0	RESULT 8 US-10-772-636-25 US-10-772-636-25 Sequence 25, Application US/10772636 Publication No. US20050042687A1 SEQUENCE 25, Application No. US20050042687A1 SEQUENCE 26, ADPLICANT: Kelly, Louise M. APPLICANT: Farlow, Deborah APPLICANT: Farlow, Deborah APPLICANT: Farlow, Deborah TITLE OF INVENTION: HERATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630, TITLE OF INVENTION: HERATOLOGICAL DISORDERS USING 918, 990, 17662, 81982, 630, TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549, TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947, TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR TITLE REFERENCE: MPIO3-015PIRNOWIM FILE REFERENCE: MPIO3-015PIRNOWIM CURRENT APPLICATION NUMBER: US 60/445,241
1312 ACCACCICCAGTIGTTANAGCTCACTCATGGACTGGAATCTAAGGATCGGAAAG 1411	2132 CCAACGGCATTGATAACGTGGAGAATGCTTAGTTTTATTGCACAGAGGTCATTTTGGGG 2191 1447 CCAACGGCATTGATAACGTGGAGAATGCTTAGTTTTTATTGCACAGAGGTCATTTTGGGG 1506 2192 GCGTGCACCGCTGGTATCATTTTTATTGCACAGAGGTCATTTTGGGG 1506 2192 GCGTGCACCGCTGTTCGGGTATTCATTTTTATTGCACAGAGTTCATTTTTTGGGG 1506 2252 TTGGGCTTCTCAGTTCAATGAAGCAATAATGAAGTATTTAACTCTTTCACTACAGTTCTT 2311 1567 TTGGGCTTCTCAGTTCAATGAAGCAATAATGAAGTATTTAACTCTTTCACTACAGTTCTT 1626 2312 GCAAGTATGCAATTAAATTACTTGACAGAGTATTTAACTCTTTCACTACAGTTCTT 1626 2312 GCAAGTATGCTATTTAAATTACTTGGCCAGGTATATTAACTCTTTTATAGTG 1686 2372 AGAAAATTTATTGGTTAAAATTACTTGGCCAGGTATAATTGCCAGTCAGT

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      FILING DATE: 2003-02-05
APPLICATION NUMBER: US (
FILING DATE: 2003-02-18
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 39 LENGTH: 3381
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ilarity 86.7%;
Conservative (
                                                            TYPE: DNA
ORGANISM: Rattus norvegicus
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APPLICANT: KUGOLDI-VGGHI, LAMIRA A.

APPLICANT: REMORIPA Rachel E.

APPLICANT: Hunter, John Joseph
APPLICANT: Hunter, John Joseph
APPLICANT: Hunter, John Joseph
APPLICANT: Hunter, John WOVEL ZATIA, 23413, 22438, 23553,
APPLICANT: Hunter, John WOVEL ZATIA, 23413, 22438, 23553,
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Publication No. US20040009553A1
GENERAL INFORMATION:
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RESULT 10 US-10-426-776-48

APPLICANT: Gluckenan, Maria Alexandra
APPLICANT: Gluckenan, Maria Alexandra
APPLICANT: Testa, Fong-Ying
APPLICANT: Rabolph-Owen, Laura A.
APPLICANT: Rabolph-Owen, Laura A.
APPLICANT: Rabolph-Owen, Laura A.
APPLICANT: Rabolph-Owen, Laura A.
APPLICANT: Rapeller-Libermann, Rosana
APPLICANT: Rapeller-Libermann, Rosana
APPLICANT: Graph-Owen, Laura A.
APPLICANT: Graph-Owen, Lorayne P.
APPLICANT: Owen, Andraw P.
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APPLICANT: Owen, Andraw P.
APPLICANT: Owen, 1403 1463 1464 TCTTAAGATGGTTTTAGAGTCTTTGCCAGAAGATGTAGGGTTTAACATTGAAATATG 1523 1524 GATCTGCCAGCAAAGGGATGGAATGTGGGATGGTAACTTATCAACATATTTTGACATGAA 1583 1344 AACAITIGACCAACTCCAGTIGITAAAGCTCACCTGGACTGCACTGAAAICTAAGGA 1403 121 AACAITICGACCAACTCCAGTIAITGAAGCTITCTCATGIGACTGCACTAAAAAACCAAAGA 180 240 1404 TCGGAAAGAATCTGTGGTTCAGGAGAAAATTCCTTTTCAGAAAATCAGCCATTTCCTTC TITCTAATAGAAAITAGAAGCTGATCCAGTIGAATTGITTGAAATCCCAGTAAAGGAAIT 1284 TATGAAAAAGAAATTTGATGCTGATCCAGTTGAATTATTTGAAATTCCAGTAAAAGAATT Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 56 SOFTWARE: FastSEQ for Windows Version 4.0 88; Length 2393; Indels Query Match
Best Local Similarity 80.1%; Pred. No. 1.1e-217;
Matches 1418; Conservative 0; Mismatches 265; Sequence 48, Application US/10426776 Publication No. US20040009553A1 GENERAL INFORMATION: TYPE: DNA ORGANISM: Rattus norvegicus SEQ ID NO 48 61 241 셤 à

1584 TCOTTTTTGGATATANTTTANAMATOTTTTAGAMATTTGGGAGGGATATATATATATATATATATA	Db 1336 ATGCATTGCACTGGTGGCTCCAGCTGCACTGTGT-CATCCATGTACGTGTGT Qy 2657 TTTTACATGGGTTGACATGCACACACACTTTCATTCATTC	OY 2717 CTGCATTTTACCAAGCAGCCTGAAGGTGAACCTGGAAAGTTGTTTGT	1763 Db 1512 ACTGTTCAAAGATTTTAAAAGTTCCAGAATGCTGCAGGGTAACTTAA 540	OY 2837 TGTATAAARTATTAGTAAGAAAAGTATTGCATACTTAGTAGATTAGAT	0y 2897 TACAAATTCAGTGCATGCTTTAGGTGTTAAGCATGAATTGTACATGTTATA 	Db 1676 CTGTCTTGGATCT-TGGATCTTGGATCTTGGTAGGTGGTAGGTGGTAGGTGGTAGGTTGGATCTGGTGCTAGGTTGGTAGGTAGGTAGGTTGGTAG	OY 3013 TATTITGTFGCCTAAAAAAAAAGCTGTTT 3043	NESULT 11 US-09-796-692-4214 Sequence 4214, Application US/09796692	2123		CURRENT APPLICATION NUMBER CURRENT FILING DATE: 2001 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-03	2303 ; PRIOR 2303 ; PRIOR 1068 ; PRIOR	PRIOR PRIOR PRIOR PRIOR PRIOR	; PRIOR APPLICATION NUMBER: ; PRIOR FILING DATE: 2000-05; ; PRIOR PPLICATION NUMBER: ; PRIOR FILING DATE: 2000-05	; PRIOR APPLICATION NUMBER: ; PRIOR FILING DATE: 2000-0: ; PRIOR FILING DATE: 2000-0	FRIOR APPLICATION FILING DATE FILING APPLICATION FILING PATE FRIOR FILING DATE	; PRIOR API ; PRIOR FII ; NUMBER OII ; SOFTWARE:	; SEQ ID NO 4214 LENUTH: 524
						1884 AGTCATATTCTGCTGGGGTGATGATACCAATGATCCTGAAAACAGAAGGAAATTG 	1944 ACTTGGAGTTAATGGTCTAATTTATGATAGGATATATGATTGGATGCCTGAACAA 			2124 TGTGGATGCCAACGCATTGATAACGTGGAGAATGCTTAGTTTTTATTGCACAGA 		2244 TATGCCTTTTGGGCTTCTCAGTTCAATGAAGCAATAATGAAGTATTTAACTCTTT1		2357 AGTCTCTTTATAGTGAGAAAATTTATTGGTTAGTAATATATAAATATTTAAACTAA. 	2417 TAAATCTTAAATGTTAAACATATGTTCATTAAAAGCATAGCACTTTGAAATTAAC 	2477 AAATAGCTCATATTTACACTTACAGCTTTTCATTTGATCAGGTCTGAAATCTTTA 	2537 TAAGGAAATGACTATGCATAATTATACCTGACCATGAAAAAATAAGTACCTCA. 	2597 AIGCATTIGCACTGGTGATTCCAACTGCACAAATCTTIGTGCCATCTIGTATATAGGTAT 2650

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AGGGTAATTTAATGTATAAATATTAGTAAGAAAAGTATGTATTGCATACTTAGTAGAA 2884
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PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-08-03
PRIOR PELING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR PILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR PILING DATE: 2000-08-07
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
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; Sequence 4214, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wanjan, Jane
; APPLICANT: Wanjan, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.8
Matches 523; Conservative
                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-040-862-4214
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US-10-057-475B-4214
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Sequence 4214, Application US/10040862

Publication No. US20030078396A1

GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Corixa Corpositions and Methods for the Detection, Diagnosis and Therapy, TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy, TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-01352008
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
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PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
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                                                                   Score 522.4; DB 9;
Pred. No. 6.1e-110;
0; Mismatches 1;
                                                                     udery Match 16.3%;
Best Local Similarity 99.8%;
Matches 523; Conservative 0
                 ; ORGANISM: Homo sapiens
US-09-796-692-4214
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US-10-040-862-4214
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APPLICANT: Gargate, Paul A.

APPLICANT: Gargate, Paul A.

APPLICANT: Marnion, Jane
APPLICANT: Retter, Marc W.

APPLICANT: Retter, Marc W.

APPLICANT: Retter, Marc W.

APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Composition and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION NUMBER: US/10/154,884B

PRIOR PELICATION NUMBER: US 60/190,479
PRIOR PELING DATE: 2000-03-17

PRIOR PELING DATE: 2000-04-28

PRIOR PELING DATE: 2000-04-28

PRIOR PELING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200,399

PRIOR PELING DATE: 2000-05-20

PRIOR PELING DATE: 2000-05-20

PRIOR PELING DATE: 2000-05-20

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481 TAGATCACAACATACAAATTCAATTCAGTGCATGCTTTAGGTGT
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                                                                                                                                                                                          Sequence 4214, Application US/10154884B
Publication No. US20040005561A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
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Matches 523; Conservative
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         APPLICANT: MCNEALL, Particia Diamne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-0144020S
CURRENT PAPLICATION NUMBER: US/10/057,475B
CURRENT PELING DATE: 2000-01-22
PRIOR PLILING DATE: 2000-01-22
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Sequence 4214, Application US/10764324

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Search completed: July 3, 2005, 00:06:53 Job time : 1867 secs

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US-10-047-855-3 3537 1 MTPSQVAFEIRGTLLPGEVF......LCGESDIHVDANGIDNVENA 672

BLOSUM62 Scoring table:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

34239544 segs, 19032134700 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Command line parameters:
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-UORTHG=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-DEV_TIMEOUT=120 -WARN TIMEOUT=3 0 -THRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

Database :

1: gb_est1:.*
2: gb_est2:.*
4: gb_est2:.*
5: gb_est4:.*
6: gb_est5:.*
7: gb_est6:.*
9: gb_gss1:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Ω	AK03064	AK05031	BC00686	AK03165	AK00956	AK04945	AK051728	BX34412	BM47843
DB	3	m	m	m	m	m	٣	Ŋ	4
% Query Match Length DB	3142	3614	3248	3578	2604	1618	2228	1006	1128
% Query Match	94.2	93.8	89.1	86.7	67.9	9.09	59.9	44.4	42.0
Score	3331.5	3318.5	3150	3066	2400	2143	2119	1570	1486.5
Result No.	1	7	e	4	2	9	7	80	9

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136	701 101 101 101 101 101 101 101

ALIGNMENTS

Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:s430401018 product.hypothetical Glycerophosphoryl diester phosphodiesterase(Glycosyl hydrolase, starch-binding domain containing protein, full insert sequence.

AK030645.

AK030645.1 GI:26326638 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) Mus musculus Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning High. Enzymol. 303, 19-44 (1999) 9279253 HTC, CAP trapper. Mus musculus (house mouse) 10349636 11042159 RESULT 1 AK030645 LOCUS DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED JOURNAL MEDLINE REFERENCE AUTHORS AUTHORS PUBMED REFERENCE TITLE

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

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S dadni, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, K., Hayatsu, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojiana, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tanaka, T., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Toya, T., Yasunishi, A., Dinect Submission

Submitted (16-JUL-2011) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Stehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:Genome-res@gec.riken.jp, Fax:81-45-503-9222, All Sandama, Inhara, Maragawa 230-0045, Japan (E-mail:Genome-res@gec.riken.jp, Fax:81-45-503-9222, All Sandama, Inhara, Maragawa 230-0045, Japan (E-mail:Genome-res@gec.riken.jp, Fax:81-45-503-9222, All Sandama, Inhara, Maragawa 230-0045, Japan (E-mail:Genome-res@gec.riken.jp, All Sandama, Inhara, Maragawa 230-0045, Japan (E-mail:Genome-res@gec.riken.jp, All Sandama, Inhara, Maragawa, Inhara, Maragawa, Inhara, Maragawa, Inhara, Maragawa, Inhara, Maragawa, Inhara, Maragawa, Maragawa, Maragawa, Inhara, Maragawa, Inhara, Maragawa, Inhara, Maragawa, Maragawa, Inhara, Maragawa, Inhara, Maragawa, Inhara, Maragawa, Maragawa, Inhara, Maragawa, Inhara, Maragawa, Inhara, Maragawa, Inhara, Maragawa, Inhara, Maragawa, Inhara, Maragawa, Inhara, Maragawa, Maragawa, Maragawa, Maragawa, Maragawa, Maragawa, Maragawa, Maragawa, Maragawa, Maragawa, Maragawa, Maragawa, Maragawa, Maragawa, Maragawa, Maragawa, Maragawa, Maragawa, Maragawa, Mara
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Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yondda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format gequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                    The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
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Nature 409, 685-690 (2001)
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TAKLAKVQENTIASLRNAASHGAAFVEFDVHLSKDFVPVYHDLTCCLTMKRKYEADP
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			1357 AAAGAATTAACATTTGACCAACTCCCAGTTATTGAAGCTTTCTCATGTGACTGCATTAAAA 1416 1357 AAAGAATTAACATTTGACCAACTCCCAGTTATTGAAGCTTTCTCATGTGACTGCATTAAAA 1416 418 SerLygAspArgLysGluSerValValGlnGluGluAsnSerPheSerGluAsnGlnPro 437 :::	458 IleLysTrpileCysGlnGlnargAspGlyMetTrpAspGlyAsnLeuSerThrTyrPhe 477 1537 ATAAAATGGATTTGCCAACACAGGGATGGAGTATGGGATGTAGATTTTT 1596 478 AspMetAsnLeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLygArg 497 1597 GATATGATTTTTGGATTATTTTAAAACTGTTTTTGGAAATTTTT 1596 498 ArgileValPheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsn 517	1657 AGAATAGTGTTTCTTCTTTTTTTGATGCAATTGTTCAATTGGTCGCAGAAGCAGAAC 1716 518 LysTyrProlleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAsp 537 1717 AAATATCCCATATTTTTGACCAAGGAAAGTTTATTTTCCCCGAACTCATGGC 1776 538 LeuArgSerArgThrThrProlleAlaMetSerPheAlaGlnPheGluAshLeuLeuGly 557	558 IleAsnValHisThrGluAspLeuLeuArgAsnProSerTyrIleGluAlaLysAla 577

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417 sSerLysAspArgLysGluSerValValGlnGluGluAsnSerPheSerGluAsnGlnPr 437
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uThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSe
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                                                                                                       -ProLeuGluSerGluIleIlelleAspAspGlyGlnPheGlyIleHisAsnGlyValGl
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      Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramateu, M. and Hayashizaki, Y. Direct Submission Submitted (16-Jul-2011) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-2. Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gec.riken.jp, URL:http://genome-gec.riken.jp/, Tel:81-45-503-922,
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Tissue was provided by William A. Held, Roswell Park Cancer
Tissue was provided by William A. Held, Roswell Park Cancer
Institute, Department of Molecular and Cellular Biology, Elm and
Carlton Streets, Buffalo, NY 14263, whose assistance we gratefully
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://genome.gsc.riken.jp/.
Location/Qualifiers

ce /organism="Mus musculus"
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Matches:
Conservative:
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Gaps:
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3614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .3601
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96.89%
92.31%
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Best Local Similarity:
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ductal carcinoma. 5 month old virgin mouse."

/clone_lib="NCI_CGAP_Mam6"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hade, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Pahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whitling, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smilus, D.E., Schnerch, A., Schein, J. E., Jones, S.J. and Marra, M.A. Green, J. Schein, J. E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 AlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaJalaLeu 40
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (27-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be for through the 1.M.A.G.B. Consortium/LLML at: http://image.llnl.gov Series: IRAK Plate: 16 Row: 1 Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetThrProSerGlnValAlaPheGluIleArgGlyThrLeuLeuProGlyGluValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Arrayed by: The I e Technologies, Inc.
CDNA Library Arrayed by: The I. M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BWA-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                     human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone has the following problem: frame shifted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3248
598
31
18
29
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Mismatches:
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Matches:
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1. 3248
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="IMAGE:3596618"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 3248)
Strausberg, R.
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88.59%
89.06%
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Best Local Similarity:
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MEDLINE
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Klausner, R. D., Collins, F. S., Wagner, L., Sheamen, C. M., Schuler, G. D.,
Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,
Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Heish, F.,
Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,
Scheetz, T. B., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,
Scheetz, F. B., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,
Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1797 GATAAATGCCCATACTGAAGACCTCCTTAGAAACCCATCCTATGTCCAAGAGGCAAAAGC 1856
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Mus musculus RIKEN cDNA 2310032D16 gene, mRNA (cDNA clone
IMAGE:3596618), containing frame-shift errors.
                                                                                                                                                                                                                       1497 AATAAAATGGATTTGCCAACACAGGGATGGAGTATGGGATGGCAACTTATCAACATATT 1556
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 3248)
ullelysTrplleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPh
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                                                                                                                                                                                                                                                                                                                                                                    GARGILeValPheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAs
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                                                                          oPheProSerLeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGl
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SOURCE
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6. O (1911) Electrolation (1917) Properties of the control of the

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mRNA linear HTC 03-APR-2004 stis cDNA, RIKEN full-length product:hypothetical esterase/Glycosyl hydrolase, otein, full insert sequence. ILVAlleuGluAenSerGlyLyeArg 497 SEGUTHTHISVALTHIALALEULYS 417 1370 hrasnasperoGluasnargargiys 597 roSerTyrlleGlnGluAlaLysAla 577 437 477 ata; Vertebrata; Euteleostomi; ognathi; Muridae; Murinae; Mus. ogluAspValGlyPheAsnIleGlu 457 uAsnSerPheSerGluAsnGlnPro rpAspGlyAsnLeuSerThrTyrPhe alGluAsnAla 672

Tue

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/tissue type="testis"
/clone Tib="RIKEN full-length enriched mouse cDNA library"
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205. 2109
/note="hypothetical Glycerophosphoryl diester
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domain containing protein (InterPro|IPR004129,
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                                                                                                                                           Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yojawa, Y., Izawa, M., Ohara, E., Watahikagi, K., Yonawa, T., Orawa, K., Tanaka, T., Matsuura, S., Kawai, J., Norasura, S., Munamatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3578)
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Nature 409, 685-690 (2001)
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Please visit our web site for further details.
URL:http://ganome.gac.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/strain="C57BL/6J"
/db_xref="RANTOM_DB:6030473012"
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, Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
subtraction of cap-trapper-selected cDNAs to
:h cDNA libraries for rapid discovery of new genes
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Ki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
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Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomizaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Salto, H., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Salto, H., Zagami, M., Tagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Shiraki, T., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yashashi, F., Tanaka, T., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Shiraki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reseggsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9212,
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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Lotter 420, 563-573 (2002) B (bases I to 1618) B (bases I to 1618) Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Harozane, T., Hayashida, K., Hayatsu, M., Hiramcto, K., Hirozane, T., Hori, Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kadani, K., Nojima, T., Miyazaki, A., Murata, M., Nokazaki, Y., Saito, R., Saito, M., Sakai, C., Sakai, K., Sakazume, N., Sakai, Y., Saito, R., Saito, R., Shiraki, T., Sano, H., Saski, D., Shibata, K., Shinagawa, A., Takaku, Akahira, S., Takaka, T., Tanaka, T., Tonaunishi, P., Takaku, Akahira, S., Takada, Y., Tanaka, T., Tonaunishi, A., Takakai, A., Takakai, T., Tanaka, T., Tonaunishi, A., Takakai, A., Takakai, T., Tonaunishi, A., Takakai, T., Tonaunishi, A., Takakai, T., Tonaunishi, A., Takakai, T., Tonaunishi, A., Tayakai, T., Tonaunishi, A., Tayakai, T., Tonaunishi, T., Tonaunishi, A.,	Muramatsu, M. and Hayashizaki, Y. Direct Submission Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Schoration Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Submiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9220, Fax:81-45-503-9216, CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.		/noce="unnamed process" //noce="unnamed process"/ /noce="unnamed process"/ /nocessive starch-binding domain containing protein /(interPro) protein /(interPro) protein /(interPro) protein //nocessive start=1 //codon start=1 //codon start=1 //codon start=1 //protein_id="BA313775.1" //db xref="ag1:2634024" //translation="MSRNSRKTIGKVRVDFIIIKPLPGYSCSMQSSFSKYWKPRIPLD //translation="MSRNSRKTIGKVRVDFIIIKPLPGYSCSMQSSFSKYWKPRIPLD //translation="MSRNSRKTIGKVRVDFIIIKPLPGYSCSMQSSFSKYWKPRIPLD //translation="MSRNSRKTIGKVRVDFIIIKPLPGYSCSWQSSFSKYWKPRIPLD //translation="MSRNSRKTIGKVRVDFIIIKFTYSCMVFLSTYFDMNVFLDIILKTYSQNS //translation="MSRNSRKTIGKVRVGHIGKNTCQHRDGVWDGNLSTYFDMNVFLDIILKTYSQNS //translation="MSRNSRKTIGKNTCQHRDGVWDGNLSTYFDMNVFLDIILKTYSQNS //translation="MSRNSRKTIGKNTCQHRDGVWDGNLSTYFDMNVFLDIILKTYSQNS //translation="MSRNSRKTIGKNTCQHRDGVWDGNLSTYFDMNVFLDIILKTYSQNS //translation="MSRNSRKTIGKNTCQHRDGVWDGNLSTYFDMNVFLDIILKTYSQNS //translation="MSRNSRKTIGKNTCGHRDGVWDGNTNPPENRRKIKEFGYNGIITYDR //translation="MSRNSRKTIGKNTCGHRDGVWDGNTNPPENRRKIKEFGYNGIITYDR //translation="MSRNSRKTIGKNTCGHRDGVWDGNTNPPENRRKIKEFGYNGIITYDR //translation="MSRNSRKTIGKNTCGHRDGVWGNTNPPENRRKIKEFGYNGIITYDR //translation="MSRNSRKTIGKNTCGHRDGVWGNTNPPENRRKIKEFGYNGIITYDR //translation="MSRNSRKTIGKNTCGHRDGVWGNTNPPENRRKIKEFGYNGIITYDR //translation="MSRNSRKTIGKNTCGHRDGVWGNTNPPENRRKIKEFGYNGIITYDR //translation="MSRNSRKTIGKNT" //translation=	Alignment Scores: 6.4e-233 Length: 1618 Pred. No.: 2143.00 Matches: 402 Score: 23 Conservative: 23 Best Local Similarity: 91.78\$ Mismatches: 13 Query Match: 3 Gaps: 0
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Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130067011 product:hypothetical G1ycerophosphoryl diester phosphodiesterase/G1ycosyl hydrolase, starch-binding domain containing protein, full insert sequence.
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Nature 409, 685-690 (2001)
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Analysis of the mouse transcriptome based on 60 60,770 full.length cDNAs
Nature 420, 563-573 (2002)
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/tissue type="spinal ganglion"
/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev Etage="12 days embryo"
                                                                                                                                                                                         Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Submitted and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7.25 Submitter, or, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9216)
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        Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nishi,K., Nomura,K., Nunazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Tagawa,A., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Tayaka,A., Takaku-Akahira,S., Takaku,M., and Hayashizaki,Y., Toya,T., Yasunishi,A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="unnamed protein product; hypothetical Glycerophosphoryl diester phosphodiesterase/Glycosyl hydrolase, starch-binding domain containing protein (Interpro|IPR004129, Interpro|IPR002044, evidence:
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Please visit our web site for further details.
Please visit our web site.
URL:http://genome.gsc.riken.jp/.
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
1. .228
/organism="Mus musculus"
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11. "HymGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BM478430.1 GI:18527472
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1. (bases 1 to 1006)

2. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

L. Unpublished (2001)

On May 1, 2003 this sequence version replaced gi:30311247.

Contact: Genoscope

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was diess of the pCMVSDORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
BX344123

BX344123 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI059YA01 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="PLACENTA COT 25-NORMALIZED"
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/note="lst strand cDNA was primed with a NotI-oligo (dT)
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digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS1AI015ZE01QP1&c=9838.r. Location/Qualifiers
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/db_xref="taxon:9606"
/clone="CS0DI059YA01"
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CB196769 901 bp mRNA linear EST 05-FEB-2003
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/clone llb="NIH MGC 135"
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Normalized full-length enriched llbrary from pooled mouse embryonic limb, maxilla and mandible, day 12.5, 13.5,
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. David Rowe
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.W.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
                                                                                                                                                                                                                            ---IysArgArg1leValPheSerSerPheAspAlaAsp-IleCysThrMet-ValArgG
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1 (bases 1 to 901)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                    TyrPheAspMetAsnLeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGly
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Location/Qualifiers
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TTCGCGTCCGAGACGATGGAACCAGATAACCTGGAACTAATCTTTGATTTTTTCGAAGAA
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      cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov.k column: 15 http://image.llnl.gov.k column: 15 High quality sequence stop: 618. Location/Qualifiers
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1. .882
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Rammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 882)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12131 row: d column: 07
High quality sequence stop: 652.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
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14.5, and 15.5 (size selected for the 0.5-1 kb fragments) Cloned directionally, priming method: Oligo-dT. CDNA enrichment: >1k bp, Average insert size 1.6k bp. Normalization (Cot value): 7.5 kb. Priming sequence: Normalization (Cot value): 7.5 kb. Priming sequence: by GACTAGTTCTAGATCGCGGCGCCC(T)3' Tissue contributed by, David Rowe. Library constructed by ResGen, Invitrogen Corp."
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TTTTTGGATATATATTTTAAAAACTGTTTTAGAAAATTCTGGGAAGAGAGAAAATAGTGTTT
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/db_xref="taxon:9606"
/clone="CS0DI059YA01"
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/tissue type="FlACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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AGENCOURT 8968328 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6491134 5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                        LeuproG]yTyrSerCysAspMetLysSerSerPheSerLysTyrTrpLysProArg11e
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                                                         CysArgHisSerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTyr
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Presion: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
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/lab_host="bH10B-T1 phage-resistant E. coli"
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/note="Organ: circulatory system; Vector: pME18S-FL3;
Site 1: Xhoi, Site 2: Xhoi; The library was prepared from polyA+ RNA from unstimulated equine peripheral blood leukocytes isolated from a healthy adult horse.
Double-stranded cDNA was cloned unidirectionally into different brall sites of the pME18S-FL3 vector (5-prime Drall site is CACCATGTG, 3-prime Drall site is CACCATGTG; XhoI excises the cDNA insert."
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Perissodactyla; Equidae; Equus.
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E (1028)
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            LeukoN2_1_G06.gl_A024 Unstimulated peripheral blood leukocytes N2 Equus caballus cDNA clone LeukoN2_1_G06_A024 5', mRNA sequence. CD466056.1 GI:31387324 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; tissue and RNA were prepared in the Department of Large
Animal Medicine, University of Georgia; sequencing done in the
Laboratory for Genomics and Bioinformatics, University of Georgia.
Sequence ends have been trimmed to exclude vector and regions below
Phred quality 16. Three-prime sequences are presented as their
reverse complement and have been trimmed to exclude polyA.
Seq primer: Sug5 (CTTCTGCTCTAAAAGCTGCG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgValLysLeuThrLeuGluGlyLeuGluGluAspAspAspAspArgValSerProThr 177
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Conservative:
Mismatches:
Indels:
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/db_xref="taxon:9796"
/clone="LeukoN2_1_G06_A024"

    .783
    /organism="Equus caballus"

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98.85$ *
98.47$
                                                                                                                                                                                                                                  Equus caballus (horse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                   Equus caballus
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Best Local Similarity:
Query Match:
DB:
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source

FEATURES

178 ValLeuHisLysMetSerAsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLys 197

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Alignment Scores:

ORIGIN

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Score:

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/tesue type="adult, 36 yr"
/lab_host="biloB"
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/clone lib="tupski dorsal root ganglion"
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1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

En (Dases I to 948)

In (Dases I to 948)

NIH-MCC http://mgc.nni.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Unpublished (1999)

Unpublished (1999)

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

Contact: Robert Strayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC. Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGENICOURT 8125917 Lupski dorsal root ganglion Homo sapiens CDNA clone IMAGE:6177333 5', mRNA sequence.
BU145581.
BY145581.1 GI:22659113
601 GCCCGTGGTGTATCATGACCTCACCTGCTGTCTGACCATGAAGAGAAATATGAAGCTGA
                                                                                                                                                                                             428 uGluasn-SerPheSerGluasnGlnProPheProSer-LeuLysMetValLeuGluSer
                                                                                                                                                                                                                                                                                                                     780 ggadartttciriticigadaricagccariticciricitadagaggiritingadarc
                                                                                                                                                                                                                                                                                                                                                                       448 LeuProGlu---AspValGlyPheAsn---IleGlulleLysTrplleCysGlnGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                        466 AspGly------MetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsnLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                661 recagiticaatiteratiteaaateeeagiaaaagaatitaceatitigaeeaacteeagniatit
                                                                                                                                                            uLysLeuThrHisValThrAlaLeuLysSerLysAspArgLysGluSerValValGlnGl
                                                      pprovalGluLeuPheGluIleProvalLysGluLeuThrPheAspGlnLeuGl
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/clone="IMAGE:6177333"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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BU145581
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                                                                                                                                                                                                                     /Organisum="ruca maccond."
/mol type="macuon: 10090"
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/note="forgan: eye, "detor: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                þe
          Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.lln.gov Plate: LLAH1.gov a column: 23 High quality sequence stop: 597.
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Mus musculus"
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Best Local Similarity:
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DB:
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APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 4005
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Matches:
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Best Local Similarity:
Query Match:
DB:
     US-11-136-527-4005
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-MODEL=frame+ p2n.model -DEV=xlh
-Q-Qcg12 1/USFTO_spool/US10047855/runat_01072005_155330_2351/app_query.fasta_1.839
-Q=/cgn2_1/USFTO_spool/US10047855/runat_01072005_155330_2351/app_query.fasta_1.839
-Q=/cgn2_1/USFTO_spool/US10047855/runat_0107787x=rnpn -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-USER=US10047855_@CGN_1 1 824 @runat_01072005_155530_2351 -NCPU=6 -ICPU=3
-NO MMAP -LAGREQUERY -NGG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                  July 3, 2005, 07:07:40; Search time 929 Seconds (without alignments) 3248.529 Million cell updates/sec
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3537
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/USO7_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/USO7_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

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19: /cgn2_6/ptodata/1/pna/USO_NEW_COMB.seq:*

11: /cgn2_6/ptodata/1/pna/USO_NEW_COMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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RESULT 2
Solution US/11136527
Sequence 4018, Application US/11136527
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For
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GENERAL INFORMATION:

APPLICANT: Venter, J. Craig

APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION EXPENSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT PILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-28

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR APPLICATION NUMBER: 60/115,693

PRIOR APPLICATION NUMBER: 60/115,693

PRIOR FILING DATE: 2000-01-12

PRIOR PILING DATE: 2000-01-12

PRIOR PILING DATE: 2000-01-12

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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                 US-11-097-143-5114; Sequence 5114, Application US/11097143; GENERAL INFORMATION:
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35.71%
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Query Match:
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; FILE REFERENCE: 031896-041000 (AM101086); CURRENT APPLICATION NUMBER: US/11/136,527; CURRENT FILING DATE: 2005-05-25; PRIOR APPLICATION NUMBER: US 60/574,294; PRIOR FILING DATE: 2005-05-26; NUMBER OF SEQ ID NOS: 362830; SOFTWARE: PatentIn version 3.2; SOFTWARE: PatentIn version 3.2; LENGTH: 2393
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Best Local Similarity:
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KENDLY ADDICATION CONTROL OF 113. Application US/11097143

GENERAL INFORMATION:

APPLICANT: Venter, J. Craig

APPLICANT: et al.

TITLE OF INVENTION: DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CLOOD728

CURRENT FILING DATE: 2005-04-04

PRIOR FILING DATE: 1999-10-19

PRIOR PLILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: 60/150, 191

PRIOR PLILING DATE: 1999-10-28

PRIOR PLILING DATE: 1999-10-28

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                                                                                                                    GluLeuGlyValAsnGlyLeuileTyrAspArg-----IleTyrAspTrpMetProGlu 617
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.765 CTGTCCAGGGAGACGCGTTCGTTTCACAACGATGATTGTTTAGAGCACCAGCCGTTTCCG 1824
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                                                                                                                     GlulleArgleuArgLeuHisTyrSerGluLysProProValSerIleThrLysLysLys 151
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2357 GGTGCCGACATGGTGGAGTTCGATGTCCAACTTAGCAAGGATCTGGTGCCAGTGGTGTAT 2298
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                                                                                                            217 TyrSerIleGlnThrMetGluProAspAsnLeuGluLeuIlePheAspPhePheGluGlu 236
                                                                                                                                                                            AspLeuSerGluHisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCys 256
                                                                                                                                                                                                                                                 LeuLeuSerSerThrlleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProlle 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                            314 LysProArg---IleProLeuAspValGlyHisArgGlyAlaGlyAsnSerThrThrThr 332
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                                                                                                                                                                                                                                                                      LyaCysArgHisSerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGlu
                                                                                                                                                                                                                                                                                                                     277 MetSerArgAsnSerArgLysThrlleGlyLysValArgValAspTyrllelleLys
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3331 CAATTACAGGTTCACAAATTCATTATGTACTGACCGACCCTATACGAGTAGAGTCCAAAA 3272
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Matches:
Conservative:
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PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
SERGID NO 5113
LENGTH: 5439
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US-11-097-143-5113
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1238 dgitaiteitedaanteetaanakit---racarretaangereteteegaangedaaki 1294 ------CAGCÁCTICCGCTIG 1003 243 264 GluSerGlyLysSerAlaGlylleLeuThrLeuProlleMetSer---ArgAsnSerArg 282 LysThrileGlyLysValArgValAspTyrileIleIleLysProLeuProGlyTyrSer 302 GlyHisArgGlyAlaGlyAsnSerThrThrThrAlaGlnLeuAlaLysValGlnGluAsn 341 920 ---GGAGTGCCCTACACACAGGGGGACATTGTCATTTCACATCACGCTGCCGCTGGAG 976 184 AsnSerLeuGlulleSerLeulleSerAspAsnGluPheLysCysArgHisSerGlnPro 203 204 GlucysglyTyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGlnThrMetGlu 223 244 GlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSerThrIleAla 263 LeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSerGluLysProPro---- 144 859 GluglyLeuGluGluAspAspAspArgValSerProThrValLeuHisLysMetSer 183 640 700 109 760 -----AspGlyGlnPheGlyIleHisAsnGlyValGluThrLeuAspSerGlyTrp 126 ---ValSerIleThriysLysLysLeuLysLysSerArgPheArgValLysLeuThrLeu 163 131 GGGCTTACCGGCGATGTGAAAGCCCTCGGCGAGTGGCAGCTGTCCAGAAGTGTGGCTCTA 490 538 100 101 ThrileAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAspVal 224 ProAspAsnLeuGluLeuIlePheAspPhePheGluGluAspLeuSerGluHisValVal |||:::||| ::: 303 CysAspMetLysSerSerPheSerLysTyrTrpLysProArgllePro---LeuAspVal -----TACAGCATGTCCAAC-----GlyProCysGlnVallleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr ||| |-----arcgccgttgggaaacccatttaggcaggccaggtcctggg CCCTGTACGGAGCTACAGTGCAGCCAGTTGGACGTCTTCGGTATTACGTCGGACAACTCC 701 GATCTAAAGCCGCAGCTGCGCGCTGGCTGAACCATGAGGCCATTCTGCAGCTCAAG -----ccccagcacgrccagcrgaagarrgrgcccgrgaagaaccgcrggccrg LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg ---- GAATCGCTGGACGAGCTCAACTGGCAGGCCACGGTGGCCCTTCAGTCC GlyvalServalGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly ---LeuGluSerGluIleIleAsp-----1004 GAGTGC-----------GAACTCCTG-977 AGGATGATGGAG-----

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GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr 100
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Matches:
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PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR PLING DATE: 1999-10-28
PRIOR PLING DATE: 1999-10-28
PRIOR PLING DATE: 1999-10-28
PRIOR PILING DATE: 1999-11-12
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                                 HisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThrMet
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TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REPERENCE: CLOOD728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT PILING DATE: 2005-04-04
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US-11-097-143-26897
; Sequence 26897, Application US/11097143
; GENERAL INFORMATION:
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	Alignment Scores: 2.52e-50 Length: 71 Pred. No.: 667.00 Matches: 20 Score: 667.00 Matches: 20 Percent Similarity: 47.24 Conservative: 12 Best Local Similarity: 29.22 Mismatches: 23 Query Match: 18.86 Indels: 13 US-10-047-855-3 (1-672) x US-11-097-143-26896 (1-7162)
164 GluGiyLeuGluGluAspAspAspAspAsgArgValSerPrOTHTVALLeuHistysMetSer 183 955GDAGGGCCTACACCAGGGGGGACTGCATCATCACACAGGCGGCGGGGGGGG	Pheaspmerasnieupheleuspileileleul Arcacaaghactriticgccdacaaggrarcc ArgargilevalpheserSerPheaspalaaspi
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DABRILLEPheGlnValGluGlnLeuGlu---ArgLeuLys 631
AspLeuLeu---ArgAsnProSer---TyrileGlnGlu 574
                                                                                                             IGLYValAsnGlyLeuIleTyrAspArgIleTyrAspTrp 614
                           ProlleAlaMetSerPheAlaGlnPheGluAsnLeuLeu 556
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Qy 575 AlaLysGlyLeuValllePheCysTrpGlyAspAspThr)	ProAspAsnLeuGluLeuIlePheAspPhePheGluGluAspLeuSerGluHisValVal
Qy 537 AspleuArgSerArgThrThrProlleAlaMetSerPheAlaGlni	AsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCysArgHisSerGlnPro
Oy AgarglevalPneSerSerPheAspalaAspilecySinrwer	145ValSerIleThrLysLysLysLeuLysLysSerArgPheArgValLysLeuThrLeu 163
	4531 TTCAATGGGGAGATGTTCCAAGTCCACGACATCGGACCTTTGAC 4578 127 LeuThrCysGlnThrGluIleArgleuHisTyrSerGluLysProPro 144 4579CCCCAGCACGTCCACGTGAAGATTGTGCCCGTGGAGAAGACGCTGGCCTG 4629
Qy 437 ProPheProSerLeuLysMetValleuGluSerLeuBroGluAsplen	4411 CCCTGTACGGAGCTACAGTGCAGCCAGTTGGACGTATTACGTCGGACAACTCC 4470 102 109 102 109 4471 GATCTAAAGCCGCAGGTGCACCGCGCTGAACCATGAGGCCATTCTGCAGGTCAAG 4530
Oy 402 PheAspGlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeul ::::::	HislysTrpGluThrHisleuGlnProArgSerIleThr ::: cGCCGTTGGGAAACCCATTTCAAGCCCAGGTCCCTGGGA
Qy 362 HisLeuSerLygAspPheValProValValTyrHisAspLeuThrC	41 LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg 60
Qy 322 GlyHisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaI	3 ProSerGlnValAlaPheGluIleArgGlyThrLeuLeuProGlyGluValPhe 20 -::-

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ieValGluPheAspVal 361
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GATCGAGTTGGATGTC 5124
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127 LeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSerGluLysProPro----
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Matches:
Conservative:
Mismatches:
Indels:
                    HATLLCANI; CL 41.

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPITITE OF INVENTION: ARRAYS, FOR DETECTING EXPITITE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE REFERENCE: CLO00728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: GO/160,191

PRIOR PLING DATE: 1999-10-28

PRIOR APPLICATION NUMBER: GO/164,769

PRIOR FILING DATE: 1999-10-28

PRIOR PLING DATE: 1999-10-28

PRIOR PLING DATE: 1999-10-28

PRIOR PLING DATE: 1999-10-28

PRIOR APPLICATION NUMBER: GO/173,693

PRIOR APPLICATION NUMBER: GO/175,693

PRIOR APPLICATION NUMBER: GO/194,831

PRIOR PLING DATE: 2000-01-12

PRIOR APPLICATION NUMBER: GO/194,831

PRIOR PLING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: GO/194,831

PRIOR PLING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SOFTWARE: PASELSO FOR WINDOWS VERSION 4.0
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LENGTH: 9667
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DRANGES, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DRANGES.
FILE REFERENCE: CLOO728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR PLICATION NUMBER: 60/161,93
PRIOR PLILON DATE: 1999-11-12
PRIOR PAPLICATION NUMBER: 60/164,769
PRIOR PAPLICATION NUMBER: 60/164,769
PRIOR PELING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PELING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PELING DATE: 2000-03-23
PRIOR PELING DATE: 2000-03-24
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ArgArg11eValPheSerSerPheAspAlaAsp11eCysThrMetValArgGlnLysGln
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8439 GGCCCAGTGCCGGATCTAAGAAAT 8462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.64e-51
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Pred. No.:
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catgatttttccattcgcgtctgcattgactcgaagacccaacgagcaaggtgatttg 1456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          568 AsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeuValIlePheCysTrpGlyAsp 587
                                                                                                       PheGlulleProValLysGluLeuThrPheAspGlnLeuGlnLeuLeuLysLeuThrHis 412
                                                                                                                                                                                       SerGluAsnGlnPro-------PheProSerLeuLysMetValLeuGluSer 447
                                                                  HisAspLeuThrCysCysLeuThrMetLysLysLysPheAspAlaAspProValGluLeu 392
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APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DRARAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REPERENCE: CL000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
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                                                                                                                                                                                                                                                                                                                                                                                             LysSerGlulleTyrProGluLeuMetAspLeuArgSerArgThrThrProIleAlaMet
                                                                                                                                                                                                                                                                                                                                                                                                                                   548 SerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnValHisThrGluAspLeuLeuArg
                                                                                                                    GlyAlaAlaPheValGluPheAspValHisLeuSerLysAspPheValProValValTyr
                                                                                                                                               ValThrAlaLeuLysSerLysAspArgLysGluSerValValGlnGluAsnSerPhe
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GENERAL INFORMATION:
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US-11-097-143-19966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 GlyProCysGlnVallleValHisLysTrpGluThrHisLeuGlnProArgSerlleThr 100
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1746 GAGGCICTGAGCTTGGAGGAGCAGAGGAGGAGAAGCTGCGTCTGCGT---
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-03-23
NUMBER OF SEC ID NOS: 43008
SOFTWARE: PRECECT ON 1996-13-13
SOFTWARE: PRECECT ON WINDER: 60/191,637
PRIOR PILING DATE: 2000-03-23
NUMBER OF SEC ID NOS: 43008
SOFTWARE: PRECECT ON WINDER: 60/191,637
PRIOR PILING DATE: 2000-03-23
NUMBER OF SEC ID NOS: 43008
SOFTWARE: PRECECT ON WINDOWS VERSION 4.0
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US-11-097-143-19966
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Best Local Similarity:
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DB:
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2958 GATCCGGGTTTGGTGCAACGGCAAAGGCACAGGTGCCCATTGTCCTGCTCTGGGGCTCG 3017
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CLOO0728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT PILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-19

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-11-2

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR PILING DATE: 1999-11-2

PRIOR PILING DATE: 1999-11-2

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR PILING DATE: 1999-11-2

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                                                    23 CysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeuLeuPro
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238 AAGAATGACTGCATTAGCTGCCTATGCCATTGCCGTCAGTTTGAGGCAAGCTTAGAGATA
                                                                                                 608 TyrasparglleTyraspTrpMet---ProGluGlnProAsnIlePheGlnValGluGln
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                                 AspThrAsnAspProGluAsnArgArgLysLeuLysGluLeuGlyValAsnGlyLeuIle
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Matches:
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SOFTWARE: FastSEQ for Windows Version 4.0
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2.11-097-143-40595
Sequence 40555, Application US/11097143
GENERAL INFORMATION:
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                                             235 GluGluAspLeuSerGluHisValValGlnGlyAspAlaLeuProGlyHisValGlyThr
                                                                                                                 255 AlaCysLeuLeuSerSerThrlleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeu
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US-11-US/143-4/DSP

Sequence 40594, Application US/11097143

GENERAL INFORMATION:

APPLICANT: Venter, J. Craig

APPLICANT: Venter, J. Craig

APPLICANT: Venter, J. Craig

APPLICANT: Venter, J. Craig

APPLICANT: Venter, J. Craig

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCI

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CLO0728

FILE REFERENCE: CLO0728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-10-28
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                                                                                  ValGluThr-----LeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArg 136
                                                                                                                                LeuHisTyrSerGluLysProProValSerIleThrLysLysLysLeuLysLysSerArg 156
                                                                                                                                                                                 PheArgValLysLeuThrLeuGluGlyLeuGluGluAspAspAspArgValSerPro 176
                                                                                                                                                                                                         574 GICCAIGIGCAGCCCAIGITTGAGGIGCCGGAGAAICCTIGIAACGAACCAGCCAAICCC 633
                                 IleThrProLeuGluSerGluIleIleAspAspGlyGlnPheGlyIleHisAsnGly 118
                                                        ATTCGAACTTGTCAGAACATGCTGAAGAACTGCGACGTCTTTGGAAAACCACACGACGAT 462
                                                                                                        GATGAAGCGAACCAGGTGGATCGCGGCTGGGCCACCACAGAGAAATTGTGCACCTGAAG 522
                                                                                                                                                       ATCTTC-----AATGCTCCATTCTGGCAAACGTCAGAAACCGAGGCTCCTGTAT 573
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grgactitactactggaggatccgcactcgccggt-----cagtatgcagactaaagg 1836
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1897 CTTCATGCTAACTCACTGCTGAACAAGCCCTCGACTATGGCATACCTGCACCAGATCAAT 1956
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.378 ATGGGAGGATCAAAACGAAAAGACCTCATTGCCGTTCCCCTGGAGGCATTTTCCTACGAT 1437
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                                                                                                                                                           GlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLysSerLysARspArgLysGlu
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                                                                                                                                SerValValGlnGluGluAsnSerPheSerGluAsnGlnProPheProSerLeuLysMet
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                                                                                                                                                                                                                                                                                                            462 CysGlnGlnArgAspGlyMetTrpAsp---GlyAsnLeuSerThrTyrPheAspMetAsn
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1856 GATTTGTACACATACGCGCATAAAGCAGGCTATGATGAACCACCGTATCATTACGGGTAC 1915
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ATTCGACCTTTGCCAAATTTCCGGTTGCGATTTGAGCCACAGCTACGAGCGTTACTGGCGC 2086
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                                                                                                                        -------HisValValGlnGlyAspAlaLeuProGlyHisValGlyThr 254
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2438 CAACTGAAGGAGGTGAAGGTCCTGCGATTCGCTGGCAGCAAAGGCTGCGATAAG-----
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                                              225 AspAsnLeuGluLeuIle------PheAspPhePheGluGluAspLeuSerGlu-
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|1403 ATTCGAACTTGTCAGAACATGCTGAAGAACTGCGACGTCTTTGGAAAACCACCACGACGAT 1462
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Mismatches:
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-02-4
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR PILING DATE: 2000-02-4
PRIOR PILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FESTSEQ for Windows Version 4.0
SEQ ID NO 40594
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18.69%
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US-11-097-143-40594
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Query Match:
DB:
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376 GTTTGGATATGCGCCAGCCAG------AGATTCTACTACCGATACCTG 417
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CLOOO728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT PILING DATE: 1999-10-05

PRIOR PELICATION NUMBER: 60/157,832

PRIOR PELICATION NUMBER: 60/160,191

PRIOR PELICATION NUMBER: 60/161,932

PRIOR PELICATION NUMBER: 60/161,932

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR FILING DATE: 1999-11-12

PRIOR PLILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 2000-01-128

PRIOR FILING DATE: 2000-01-128

PRIOR FILING DATE: 2000-01-128

PRIOR FILING DATE: 2000-01-224

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SOFTWARE: PRESEQ for Windows Version 4.0

SEQ ID NOS: 43008

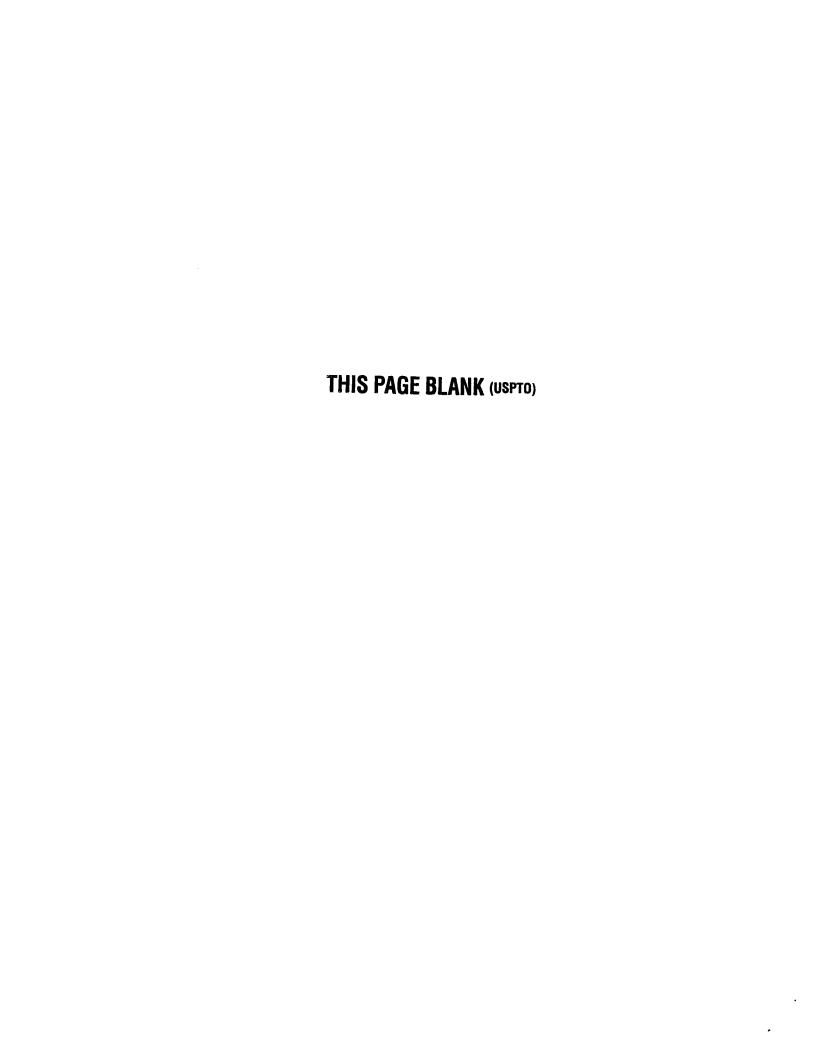
SEQ ID NOS: 43008
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242 TTGGAACGCCTGAAGCAAGAATTGCCAGAGCTTAAGAGCTGTTTGTGTCCCACTGTTAGC
                                                        ArgPheValProSerSerLeuCys---GlyGluSerAspileHisValAspAlaAsnGly
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                  Sequence 33686, Application US/11097143
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
                                                                                                             666 ileAspAsnValGluAsnAla 672
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ORGANISM: DROSOPHILA
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Best Local Similarity:
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Sequence 1279, Application PC/TUSOS00517
Sequence 1279, Application PC/TUSOS00517
GENERAL THE OHIO STATE UNIVERSITY
TITLE OF INVENTION: METHODS OF USING DATABASES TO CREATE GENE-EXPRESSION MICROARRAYS,
TITLE OF INVENTION: MICROARRAYS CREATED THEREBY, AND USES OF THE MICROARRAYS
TITLE REPRENCE: 18225-04130
CURRENT APPLICATION NUMBER: PCT/USOS/00517
CURRENT PILING DATE: 2004-01-07
PRIOR PILING DATE: 2004-01-08
NUMBER OF SEQ ID NOS: 3859
SOFTWARE: PATCHIN VERSION 3.3
SOFTWARE: PATCHIN VERSION 3.3
SEQ ID NO 1279
LENGTH: 693
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                                                                                                                                                                                                   2837 GTAAGCGTGCAGGATGTTGCCGTGAGGTTTTGCAACAGTCTGGAGTTCCTTGGGCTGACC 2896
                                                                                                                                                                          580 LeuValilePheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLygLeuLyg 599
                                                                                                                                                                                                                                               600 GluLeuGjyvajAsnGjyLeuijeTyrAspArgileTyrAspTrpMetProGluGlnPro 619
                                                                                                                                                                                                                                                                                                                   620 AsnilePheGlnValGluGlnLeuGluArgLeuLysGlnGluLeuProGluLeuLysSer 639
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; ORGANISM: Equus caballus
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	472 AGAGTGGCTCGAATGCTGCAGACCTACGGGATCTCCCCGGGTCTGGACATCTTC 531	DD 1395 TARIGICARGGATGTGAGCCCAAAAACACAGAATTTCCCAAAAACTCTCGGAGGTTTTGA 1454 On AAA NGATANDYGTNABAAGATGTTABAAAAAAAAAAAAAAAAAAAAAAAAA
	108 IleaspaspGlyGlnPheGlyIleHisasnGlyValGluThrLeuAspSerGlyTrpLeu 127 ::: 532 GGGAGGCCTACCCCGTCTCAGTGGGGGATTCTATCTGGAACGCGATTGGTTTC 588	1455 GGCCTACCCAAAACACTGGGGACTTCTGGAGGATAAAGTGGCCGCAAAT-AA
	ile	466 pGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMet-AsnLeuDheLeuAspIleI
	589 CAGTACGAGTACGAGTAGAGCTAAAATTCGTCTGGCAGGATCATATTGCTATTTCT 645	DD 1508 TGGCTTCTGGTGTGCCGGAATCCCACGCGAGTTTGAACAAAACATTTACGTGGAAAAA 1567
	148 ThrLysLysLysLeuLysLysLysLerArgPheArgValLysLeuThrLeuGluGlyLeuGlu 167	1568 TICTACAGATCACGATTCATCATGGGTGTGGACGTCCACTAATCTTCGCCAGCTTTGATG
	GluAspAspAspAspArgValSerProThrValLeuHisLysMetSerAsnSerLeuGlu	Oy 506 laAspileCysThrMetValArgGlnLysGlnAsnLysTyrProlleLeuPheLeuThrG 526
	188 IleSerLeulleSerAspAsnGluPheLysCysArg-HisSerGlnProGluCysGl 206	526 InGlyLysSerGlulleTyrProGluLeuMetAspLeuArgSerArgThrThrProlleA
	- 5505 - 100	DD 1088 IIGGCAAGICICAGAIIIGGGAIGAGIAAAIGGAICIGAGGGCACACAGAIIICCAGCAAAG 1/4/ Qy 546 laMetSerPheAlaGlnPheGluAsnLeuLeuGiQlylleAsnValHigThrGluAspLeuL 566
	206 YTYTG1YLeuGlnPro 217 778 TACACACAGGCACCATTGTTGTTTTCCGGATTTACCAACCGCTGGACAC-TACAATGC 836	Db 1748 CCATCAACTTCGTTCAGTCCGCAGAAATTTTGGGAACAGCTCTGCACGTGGAAAACTTCC 1807
	hePh	Qy 566 euArgAsnProSerTyrIleGlnGlualaLysAlaLysGlyLeuValIlePheCysTrpG 586
	837 CCTTCGCTTGTCTATTTATCAGGCATCAAGAGATCTCCAGTTA	586 1yAspAspThrAsnAspProGluAsnArgArgLysLeuLysGluLeuGlyValAsnGlyL
	880TCCCTTGGAGAGGGGTATTTCCGGATCAAATCAAGGGC 921	1868 GTAACGATATGCAAGATGAACATCTTCTGGAGCAATTTAGAGCTCTGGATGTGACGGGTC
	rAlaCysLeuLeuSerSerThr1leAlaGluSerGlyLysSerAlaGly1leLeuThrLe	Qy 606 eulleTyrAspArgIleTyrAspTrpMetProGluGlnProAsnI 621
	274 uProileMetSerArgAsnSerArgLysThrileGlyLysValArgValAspTyrIlell 294	621 lePheGlnValGluGlnLeuGluArgLeu
	::: ::: :::::	Db 1982 TTTCCGGGCCCCACAACTTATGGAACTA 2010
	294 elleLysProLeuProGlyTyrSerCysAspMetLysSerSerPheSerLysTyrTr 313 	RESULT 15 US-11-097-143-33685 ; Sequence 33685, Application US/11097143 ; GENRRAL, INFORMATION:
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-		; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID ; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE ; TITLE OF INVENTION: DEPORTED THE STATES
•	332 rAlaGlnLeuAlaLysValGlnGluAsnThrIleAlaSerLeuArgAsnAlaAlaSerHi 352 .:: 5::: ACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	REFERENCE: CL00(NT APPLICATION)
•		; PRIOR FILING DATE: 1999-10-05
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•		FILING DATE:
•		; PRIOR FILING DATE: 1999-11-12 ; PRIOR PEPLICATION NUMBER: 60/173,383
	392 UPREGIULIPETORALLYSGIULEUTTEPREASDGINLEUGULTULEULEULTREH 412 1299 ACGGTTTGTGCTAATAAGGAAACTTACTACTACTGGAACTCAAGGCCAGCC 1349	; PRIOR FILING DATE: 1995-12-28; PRIOR APPLICATION NUMBER: 60/175,693; PRIOR FILING DATE: 2000-01.10
	412 sValThrAlaLeuLysSerLysAspArgLysGluSerValValGluGluGluAsnSerPh 432	
_	1350 GGTGTTTATCCTCAAACGTTGGACCGTCCAGGAATACACCAATCT 1394	35K: 00/131, 30-03-23 43008
	432 eSer	; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 33685

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| AGAGTGGCTCGAATGCTGCAGACCTACGAGATCTACCGCTCCCCGGGTCTGGACATCTTC 1531
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                                                                                                                              14 LeuLeuProGlyGluValPheAlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsn
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316 CTCGAGAGGCTCTACCCCTCAAGGAGCAGGAGAGAGGCGCGCACCAAGTGGTATCTGAGG
                                                                                                                                                                                                   AlaThrileValLeuSerArgGlyValSerValGlnTyrArgTyrPheLysGlyTyrPhe
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; LENCTH: 4100
; TYPE: DNA
; ORGANISM: DROSOPHILA
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8868 GTAACGATATGCAAGATGAACATCTTCTGGAGCAATTTAGAGCTCTGGATGTGAGGGTC 2927 2454 2567 586 jyaspaspThrasnaspProGluasnargargLysLeuLysGluLeuGlyValasnGlyL 606 412 2350 GGTGTTTATCCTC------AAACGTTGGACCGTCCAGGAATACACCAATCT 2394 621 .942 CCCCATCTTTGCTAGTTTACAAAATTTGGCCATTGGGGAGATCACGTTGCCATATTTGGT 2001 332 pGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMet-AsnLeuPheLeuAsplleI jaAspileCysThrMetValArgGlnLysGlnAsnLysTyrProlleLeuPheLeuThrG 526 lnGlyLysSerGlulleTyrProGluLeuMetAspLeuArgSerArgThrThrProlleA 546 laMetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnValHisThrGluAspLeuL euArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeuValIlePheCysTrpG aaaacaacaccagcaagtcaacttggccrtggatctgcagcagtctcttttttatggg euileTyrAspArgile-----TyrAspTrpMetProGluGlnProAsnI 2395 TAATGTCAAGGATGTGAGCCAAAAACACAGAATTTTCCCAAAACTCTCGGAGGTTTTTGA GCATGGATTTGGATTTTACACCTCAGACACAGATCGCTCTGTAAGGGATCGCTTTGATTT plysProArg11ePro---LeuAspValG1yHisArgG1yAlaG1yAsnSerThrThrTh uPheGluIleProValLysGluLeuThrPheAspGlnLeuGlnLeuLeuLysLeuThrHi ACGGTTTGTGCTAATAAGGGAACTTACCTACTCGGAA-----CTCAAGGCCAGCCG 412 svalThrhlaiceurysSerLysAspArgiysGluSerValvalGluGluAsnSerPh 2122 ATCTTCA---ACGAGTCTTACGGAGAGCACCATCGAAGTTATCTGGCAGTTCTGAAGGC sGlyAlaAlaPheValGluPheAspValHisLeuSerLysAspPheValProValValTy rHisAspLeuThrCysCysLeuThrMetLysLysLysPheAspAlaAspProValGluLe eSer------GluAsnGlnProPheProSerLeuLysMetValLeuGl elleLysProLeuProGlyTyrSerCys---AspMetLysSerSerPheSerLysTyrTr ralaglnLeualaLysValglnGluAsnThrIleAlaSerLeuArgAsnAlaAlaSerHi ::: |||||||||| 621 lePheGlnValGluGlnLeuGluArgLeu 630

Search completed: July 3, 2005, 13:08:50 Job time: 1006 secs



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Minimum DB seq length: 0
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Listing first 45 summaries

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Published Applications Ma:*

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Pred. No. is the number of results predicted by chance to have a

APPLICANT: Healy, Ailean
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TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
TITLE OF INVENTION: 14472, 1762, 19290, 21620, 21689, 28899, 53659, 64549,
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TITLE OF INVENTION: 9303, 9465, 13913, 13908, 14605, 16652, 1521, 6662, 13913, 12405 OR
TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR

Farlow, Deborah

APPLICANT:

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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33 298 8.4 1319 34 291 8.2 401 35 286.5 8.1 1724 36 286.5 8.1 1724 37 282 8.0 1399 38 282 8.0 1399 40 273 7.7 1523 40 273 7.7 1604 41 272.5 7.7 1949 43 259 7.3 323 44 255 7.2 151 45 251.5 7.1 1191	18 IIS-10-425-114-27639	27639
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37 282 8.0 1399 38 282 8.0 1637 40 273 7.7 1604 41 272.5 7.7 1949 42 271.5 7.7 1164 43 259 7.3 323 44 255 7.2 151 45 251.5 7.1 1191	20 US-10-425-115-162869	162869.
38 282 8.0 1637 39 273 7.7 1523 41 272.5 7.7 1949 42 271.5 7.7 1949 43 259 7.3 323 44 255 7.2 151 45 251.5 7.1 1191	18 US-10-425-114-22946	2294
39 273 7.7 1523 40 273 7.7 1604 42 271.5 7.7 1649 43 259 7.3 323 44 255 7.2 151 45 251.5 7.1 1191	20 US-10-425-115-168094	168094,
40 273 7.7 1604 41 272.5 7.7 1949 42 271.5 7.7 1164 43 259 7.3 323 44 255 7.2 151 45 251.5 7.1 1191	18 US-10-425-114-22914	22914
41 272.5 7.7 1949 42 271.5 7.7 1164 43 259 7.3 323 44 255 7.2 151 45 251.5 7.1 1191	20 US-10-425-115-34867	34867
42 271.5 7.7 1164 43 259 7.3 323 44 255 7.2 151 45 251.5 7.1 1191	20 US-10-739-930-755	75
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251.5 7.1 1191	US-09-864-761-1911	191
	9 US-10-437	Sequence 226
	ALIGNMENTS	
US-10-772-636-25		
; Sequence 25, Application US/107/263 : Publication No. US20050042687A1	/107/2636 87A1	
GENERAL INFORMATION:		
; APPLICANT: Kelly, Louise M.		

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ValGlyHisArgGlyAlaGlyAsnSerThrThrThrAlaGlnLeuAlaLyeValGlnGlu 340
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                                                                                                                                                                                           GlulysProProValSerIleThrLysLysLeuLysLysLysSerArgPheArgValLys
                                           uAspAspAspAspArgValSerProThrValLeuHis
                                              LysMetSerAsnSerLeuGlulleSerLeulleSerAspAsnGluPheLysCyaArgHis
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         FILE REFERENCE: MP103-015PIRNOMNIM
CURRENT APPLICATION NUMBER: US/10/772,636
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, NAME/KEY: CDS

, LOCATION: (1).

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1501 TTTCTTCATTGATGATGATATTTGCACAATGGTTCGGCAAAGCAGAACAATATCCG 521 IleleuPheleuThrGlnGlyLysSerGlulleTyrProGluleuMetAspLeuArgSer	DD	58	Oy 581 ValllePheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLysLeuLysGlu 600	Oy 601 LeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGlnDroAsn 620	Qy 621 IlePheGlnValGluGlnLeuGluargLeuLysGlnGluLeuProGluLeuLysGerCys 640 Db 1861 ATATTCCAAGTGGAGCAATTGGAACGCCTGAAGCAGAATTGCCAGAGCTTAAGAGCTGT 1920	Qy 641 LeuCysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHis 660 Db 1921 TTGTGTCCACTGTTAGCCGCTTTGTTCCTCATCTTTGTGTGGGAGTCTGATATCCAT 1980	Qy 661 ValAspAlaAsnGlyIleAspAsnValGluAsnAla 672 Db 1981 GTGGATGCCAACGCCATTGATAACGTGAGATGCT 2016	RESULT 2 US-10-047-855-4 ; Sequence 4, Application US/10047855	; Publication No. US20030165863A1 ; GENERAL INFORMATION: ; APPLICANT: Chiang, Lillian Wei-Ming ; TITLE OF INVENTION: NARCIG and NARCIG, Programmed Cell	TITLE OF INVENTION: Death-Associated Molecules and Uses Thereof FILE REFRENCE: 35800/242056 CURRENT APPLICATION NUMBER: US/10/047,855 CURRENT FILING DATE: 2002-01-15	; PRIOR APPLICATION NUMBER: US 60/262,306 ; PRIOR FILING DATE: 2001-01-16 ; NUMBER OF SEQ ID NOS: 16 ; SOFTWARE: PastSEQ for Windows Version 4.0	; SEQ ID NO 4 ; LENGTH: 3206 ; TYPE: DNA ; ORGANISM: Homo sapiens	FEATURE: NAME/KEY: CDS LOCATION: (145)(2163) NAME/KEY: misc_feature	; LOCATION: (1)(17) ; OTHER INFORMATION: Vector sequence US-10-047-855-4	Alignment Scores: 0 Length: 3206 Score: 3537.00 Matches: 672 Percent Similarity: 100.00\$ Conservative: 0	: 100.00% Mismatches: 100.00% Indels: 16 Gaps:	US-10-047-855-3 (1-672) x US-10-047-855-4 (1-3206) Qy 1 MetThrProSerGlnValAlaPheGluIleArqGlyThrLeuLeuProGlyGluValPhe 20

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Sequence 34, Application US/10426776; Publication No. US20040009553A1; GENERAL INFORMATION:
APPLICANT: Glucksman, Maria Alexandra APPLICANT: Williamson, Mark J. APPLICANT: Tsia, Fong-Ying; APPLICANT: Rudolph-Owen, Laura A. APPLICANT: Rapeller-Libermann, Rosana; APPLICANT: Meyers, Rachel E.

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APPLICANT: Wood, Andrew
APPLICANT: Wood, Andrew
APPLICANT: Wood, Andrew
APPLICANT: Wood, Andrew
TITLE OF INVENTION: 25212, MARC 21, MARC 104, MARC 11,
TITLE OF INVENTION: 25212, MARC 21, MARC 20, MARC 20, MARC 21,
TITLE OF INVENTION: NARCIA, MARC 12, MARC 19, MARC 20, MARC 26, MARC 27, MARC 20, MARC 21,
TITLE OF INVENTION: ANDREWING MARC 14, MARC 19, MARC 10C, MARC 26, MARC 30, MARC 6, MARC 31, MARC 26, MARC 27, MARC 29, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, MARC 10C, M
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Chiang, Lillian Wei-Ming
Hunter, John Joseph
Wood, Andrew
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101 ProLeuGluSerGlu1leIleIleAspAspGlyGlnPheGly1leHisAsnGlyValGlu 120	S ACTCTGGATTCTGGATGGCTGACTGTCAGACTGAAATAAGATTACGTTTGCATTATTCT 1 GluLysProProValSer1leThrLysLysLysLysLysLysSerArgPheArgValLys	565 GAAAAACCICCIGICICAATAACCAAGAAAAATTAAAAAATCTAGATTTAGGGTGAAG 624 161 LeuThrLeuGluGlyLeuGluGluAspAspAspArgValSerProThrValLeuHis 180		201 SerGinProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGln 220 	221 ThrMetGluProAspAsnLeuGluLeullePheAspPhePheGluGluAspLeuSerGlu 240 	241 HisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSer 260 	261 ThrileAlaGluSerGlyLysSerAlaGlylleLeuThrLeuProlleMetSerArgAan 280 	281 SerArgLysThrileGlyLysValArgValAspTyrileileilelysProLeuProdly 300 	301 TyrserCysaspMetLysSerSerPheSerLysTyrTrpLysProArglleProLeuasp 320 	321 ValGlyHisArgGlyAlaGlyAsnSerThrThrThrAlaGlnLeuAlaLysValGlnGlu 340 	341 ABNThrileAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAsp 360 	361 ValHisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThr 380 	381 Metlyslyspheaspalaaspprovaldluleuphegluileprovallysgluleu 400 	401 ThrPheAspGlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAsp 420 	421 ArgLysGluSerValValGluGluGluAsnSerPheSerGluAsnGlnProPheProSer 440	441 LeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLygTxp 460	

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LeuGlyValAsnGlyLeuileTyrAspArgileTyrAspTrpMetProGluGlnProAsn
                                                                                                                                                                                             IlepheGlnValGluGlnLeuGluArgLeuLysGlnGluLeuProGluLeuLysSerCys
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US-09-814-353-21000
US-09-814-000, Application US/09;
Sequence 21000, Application US/09;
Publication No. US20030165831A1;
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Ender
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND FILE REFERENCE: MRL-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/210,610
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-12-21
NUMBER: OF SEQ ID NOS: 22037
SOFTWARRE: FASESEQ for Windows Version 4.0
SEQ ID NO 21000
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| LOCATION: 3490, 3491, 3492, 3493, 3494, 3495, 3496, 3497, 3498, 3499
| OTHER INFORMATION: n = A,T,C or G
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APPLICANT: Schlegel. Robert

APPLICANT: Endege, Wilson

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: HUMAN PROSITE CANCER

TITLE OF INVENTION: HUMAN PROSITE CANCER

TITLE OF INVENTION: HUMAN PROSITE CANCER

TITLE OF INVENTION: HUMAN PROSITE CANCER

TITLE OF INVENTION: HUMAN PROSITE CANCER

TITLE OF INVENTION: HUMBER: 09/785,276

PRIOR PELICATION NUMBER: 06/183,319

PRIOR FILING DATE: 2003-02-07

PRIOR FILING DATE: 2000-02-17

PRIOR PELICATION NUMBER: 60/207,454

PRIOR FILING DATE: 2000-06-25

PRIOR PELICATION NUMBER: 60/211,314

PRIOR PELICATION NUMBER: 60/211,314

PRIOR PELICATION NUMBER: 60/211,314

PRIOR PELICATION NUMBER: 60/219,007

PRIOR PELICATION NUMBER: 60/219,007

PRIOR PELICATION NUMBER: 60/215,281

PRIOR PELICATION NUMBER: 60/215,281

PRIOR PELICATION NUMBER: 60/215,281

PRIOR PELICATION NUMBER: 60/215,381

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LOCATION: 3490, 3491, 3492, 3493, 3494, 3495, 3496, 3497, 3498, 3499
OTHER INFORMATION: n = A,T,C or G
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Matches:
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND THERE
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERE
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE
CURRENT APPLICATION NUMBER: 09/785,276
PRIOR PAPLICATION NUMBER: 09/785,276
PRIOR PILING DATE: 2000-02-17
PRIOR PAPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-01-2-3
SOFTWARE: FRAESEQ for Windows Version 4.0
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i LOCATION: 3490, 3491, 3492, 3493, 3494, 3495, 3496, 3497, 3498, 3499
i CTHEN INFORMATION: n = A,T,C or G
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Best Local Similarity:
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Pred. No.:
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US-10-357-930-29632
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| Sequence 39 Application US/10426776
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| GENERAL INFORMATION |
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  PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrPro
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              TITICITCATTAGATGCAGATATTTGCACAATGGTTCGGCAAAAGCAGAACAATATCCG
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PRIOR FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: 09/773,426
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 1999-10-22
PRIOR FILING DATE: 1999-10-22
Remaining Prior Application data removed - Sc
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 39
LENGTH: 3381
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PRIOR APPLICATION NUMBER: 09/773,426
PRIOR FILING DATE: 2001-01-31
PRIOR PELLING DATE: 2001-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 1999-10-22
Remaining Prior Application data removed - St
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 2393
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| Sequence 48, Application US/10426776
| Sequence 48, Application US/10426776
| Sequence 48, Application US/004000953A1
| GENERAL INFORMATION:
| APPLICANT: Glockeman, Maria Alexandra
| APPLICANT: Glockeman, Mark J. |
| APPLICANT: Williamson, Mark J. |
| APPLICANT: Williamson, Mark J. |
| APPLICANT: Radolph-Owen, Laura A. |
| APPLICANT: Radolph-Owen, Laura A. |
| APPLICANT: Chiang Lillian Wei-Ming Mei-Ming APPLICANT: Chiang Lillian Wei-Ming Mei-Ming APPLICANT: Chiang Lillian Wei-Ming Mei-Ming APPLICANT: Chiang Lillian Wei-Ming Mei-Ming APPLICANT: Chiang Lillian Wei-Ming Mei-Ming APPLICANT: Chiang Lorayne P. |
| APPLICANT: Chiang Lillian Wei-Ming Mei-Ming APPLICANT: Chiang Lillian Wei-Ming Mei-Ming Mei-Ming Mei-Ming Lorayne P. |
| TITLE OF INVENTION: 25278, 26212, NARC 25, NARC 6, NARC 19, NARC 11, TITLE OF INVENTION: NARC 144, NARC 15, NARC 165, NARC 10C, NARC 10C, NARC 10C, NARC 11, TITLE OF INVENTION: S1, NARC 29, NARC 10C, NARC 10C, NARC 11, TITLE OF INVENTION: 20, NARC 20, NARC 10C, NARC 10C, NARC 11, TITLE OF INVENTION: 86004 AND 3222 MOLECTLES AND USBES THEREFOR FILING DATE: 2003-04-30 |
| TITLE OF INVENTION NUMBER: US/10/426,776 |
| PRIOR APPLICATION NUMBER: US/10/426,776 |
| PRIOR APPLICATION NUMBER: 10/105,992 |
| PRIOR PILING DATE: 2000-02-28 |
| PRIOR APPLICATION NUMBER: 09/406,62 |
| PRIOR PILING DATE: 2000-02-28 |
| PRIOR PILING DATE: 2000-02-28 |
| PRIOR PILING DATE: 2000-02-28 |
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                                                                                                                                                          Sequence 1849, Application US/09998598
; Sequence 1849, Application US/09998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
    APPLICANT: Stolk, John A.
; APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Chenault, Redelein Joy
; TITLE OF INVENTION: DIAGNOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSITIONS AND COLON CANCER
; FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/0998,598
; CURRENT APPLICATION NUMBER: US/0999,598
; SEQ ID NO 1849
; LENGTH: 471

MENTER COLINA INVENTION DISCLOSURE DATAbase
; SEQ ID NO 1849
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Lee, John
APPLICANT: Lille, James
APPLICANT: Lille, James
TITLE OF INVENTION: NOVE GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-0068
CURRENT FILING DATE: 2001-03-21
PRIOR PLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
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Matches:
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                                                                                                                                                                                      ; Sequence 16669, Application US/09814353; Publication No. US20030165831A1; GENERAL INFORMATION:
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410 223

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APPLICANT: Algate, Paul Applicant: Algate, Paul Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Mandia Applicant: Mandia Applicant: Wangi Adjum
APPLICANT: Carear, Lauren
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Matches:
Conservative:
Mismatches:
Indels:
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; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
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; OTHER INFORMATION: n
US-10-057-475B-8067
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Best Local Similarity:
Query Match:
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US-10-057-475B-8067
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PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR PILING DATE: 2000-08-04
PRIOR PILING DATE: 2000-08-07
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FASESEQ for Windows Version 3.0
SSETWARE: 436
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LOCATION: (188)
COTHER INFORMATION: n=A,T,C or G
FEATURE:
NAME/KEY: unsure
LOCATION: (213)
OTHER INFORMATION: n=A,T,C or G
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; OTHER INFORMATION: n=A,T,C or US-10-040-862-8067
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NAME/KEY: unsure
LOCATION: (11)
OTHER INFORMATION: n=A,T,C
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OTHER INFORMATION: n=A,T,C
                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: unsure
LOCATION: (184)
OTHER INFORMATION: n:
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NAME/KEY: unsure
LOCATION: (298)
OTHER INFORMATION: n
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NAME/KEY: unsure
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US-10-047-855-3 (1-672) x US-10-057-475B-8067 (1-436)
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qq	1 CTGGCTAAAGNTCAANAAAATACTATTGCTTCTTTAAGAAATGCTGCTAGTCATGGTGCA 60
ò	355 AlaPheValGluPheAspValHisLeuSerLyeAspPheValProValValTyrHisAsp 374
QQ	61 GCCTTTGTAGAATTTGACGTACACCTTTCAAAGGACTTTGTGCCCCGTGGTATATCATGAT 120
ò	375 LeuThrCysCysLeuThrMetLysLysPheAspAlaAspProValGluLeuPheGlu 394
qq	121 CTTACCTGTTGTTGAAAAAAAAAAATTTGATGCTGATACAGTTGAATTTTGAA 180
ò	395 IleProValLysGluLeuThrPheAspGlnLeuGlnLeuLysLeuThrHisValThr 414
qq	181 ATTNCAGNAAAAGAATTAACATTTGACCAACTNCAGTTGTTAAAGCTCACTCATGTGACT 240
ò	415 AlaLeuLysSerLysAspArgLysGluSerValValGlnGluGluGuAsnSerPheSerGlu 434
qq	241 GCACTGAAATCTAAGGATCGAAAAGAATCTGTGGTTCAGGAGGAAAATTCCTTTTCANAA 300
ò	435 AsnGlnProPheProSerLeuLysMetValLeuGluSerLeuProGluAspValGlyPhe 454
q	301 AATCAGCCATTTCCTCTTAAGAIGGTTTTAGAGTCTTTGCCANAAGAIGTTT 360
ò	455 AsnileGluileLysTrpileCysGlnGlnArgAspGlyMetTrp-AspGlyAsnLeuSe 474
qq	361 AACATTGAAATAAAATGGATCTGCCAGCAAAGGGATGGAATGTGGGGATGGTAACTTATC 420
È	474 rThrTyrPheAspMet 479
ą	421 AACATATTTGACATG 436

Search completed: July 3, 2005, 13:26:08 Job time : 1109 secs



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2569 GGGCTTACCGGCGATGTGAAAGCCCTCGGCGAGTGGCCAGTGTCCAGAAGTGTGGCTCTA 2510
                                                                                               Sequence 2289, Ap
Sequence 498, App
Sequence 305, App
Sequence 259, App
Sequence 259, App
Sequence 801, App
Sequence 801, App
                                                                                                                                                                                                                                      Sequence 4030, Apple Sequence 355, Apple Sequence 33, Appl Sequence 11, Appli Sequence 2260, Apple Sequence 222, Apple Sequence 202, Apple Sequence 12, Appli Sequence 11, Appli Sequence 638, Appli Sequence 638, Appli
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Sequence 1, Appli
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Sequence 3, Appli
Sequence 5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1

US-09-270-767-11893/c

Sequence 11893, Application US/09270767

Factor No. 6703491

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOTTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 ProSerGlnValAlaPheGluIleArg-----GlyThrLeuLeuProGlyGluValPhe 20
                                                                                                                                                                                                Sequence 1448, A Sequence 1076, A Sequence 4030, A Sequence 565, A Sequence 33, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2629 CCCACTCTGCGGGAGTTCAATGTGCGGCTGGAGGATTCCCCTGGCCGCCGAGGAGCGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 AlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaJaLeu ::: ||||||||||
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Sequence
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US-10-047-855-3 (1-672) x US-09-270-767-11893 (1-2786)
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Mismatches:
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US-09-643-990A-1
US-09-489-039A-3679
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US-08-717-515-5
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Query Match:
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LENGTH: 2786
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  124
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    Score:
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-MODEL=frame+ p2n.model -DEV=x1h
-MODEL=frame+ p2n.model -DEV=x1h
-Q=/cgn2_1/USFTO_spool/US10047855/runat_01072005_155529_2259/app_query.fasta_1.839
-Q=/cgn2_1/USFTO_spool/US10047855/runat_01072005_155529_2259/app_query.fasta_1.839
-DB=15sucd_Patente NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LAGDECL=0
-LOOPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-NOBE-LOCAL -OUTFMT=pcc -NORM=ext -HEAPSIZE=500 -MINLENE=0 -MAXLEN=200000000
-USRB=US10047855_GCGN_1 1_177 @runat_01072005_155529_2259 -NCFU=6 -ICFU=3
-NO MANAP -LARGEQUERY -NGG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27552, A Sequence 1858, Ap Sequence 1148, Ap Sequence 1012, Ap Sequence 2048, Ap Sequence 71, Appl Sequence 9, Appliance 1900, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11893, A
Sequence 27552, A
                                                                                             July 3, 2005, 06:49:10 ; Search time 307 Seconds (without alignments) 3581.687 Million cell updates/sec
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                                                                                                                                                                                 MTPSQVAFEIRGTLLPGEVF.....LCGESDIHVDANGIDNVENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ued_Patents_NA:*
/cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq;*
/cgn2_6/ptodata/1/ina/6A_COMB.seq;*
/cgn2_6/ptodata/1/ina/6B_COMB.seq;*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq;*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq;*
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                      nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-270-767-11893
US-09-270-767-27552
US-09-248-796A-1858
US-09-328-352-1388
US-09-328-352-1148
US-09-543-681A-2048
US-09-543-681A-2048
US-09-247-155-71
US-09-105-697-9
US-09-105-697-9
US-09-22-991A-1900
US-09-22-991A-1900
                                                                                                                                                                                                                                                                                                                         hits satisfying chosen parameters:
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SUMMARIES

Issued

Database :

Length

Query Match

Result

N_O

2786 1180 2421 1161 720 14570 759 1487 1629 2682 2682 1173

654 462 163 153 131.5 131.5 131.5 128.5 126.5

1202784 segs, 818138359 residues

, Xgapext , Ygapext , Fgapext , Delext

BLOSUM62 Xgapop 10.0 , Ygapop 10.0 , Fgapop 6.0 , Delop 6.0 ,

US-10-047-855-3 3537

Title: Perfect score:

Sequence:

protein

Run on:

Scoring table:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Total number

Searched:

us-10-047-855-3.rni

Leafitosiumanspinitulylussemicualityis	Db 1645 CATTTGACTGCTGATGGTGTGCTGTGALTTATCACGATT Qy 382 LysLysPheAspAlaAspProValGluLeuPheGlul ::: ::: ::	Qy 402 Db 1525	Qy 422 Db 1483	Qy 437 Db 1429	Oy 456 Db 1369	Qy 476 Db 1315	Qy 496 Db 1255	OY 516 HASHLYSTY FILLE CONTROLL	Qy 536 taspleuargSerargThrThrProllealaMetSerPh	Oy 556 uGly1leAsnValHisThrGluAspLeuLeuArgAs	76 Qy 574 UAIALYSAIALYSGIYLEUVAIIIEPheCYSTrpGIYAB 3	7 Qy 594	4 Db 955	3 Oy 631	Db 836	 _		-
	41 LeuprogluAsnAspThrGlyGluSerMetLeuTrpLysAlathritateValleuserArg %0	TGCCGCCAGCTGGAGTACCGCTACTTTGTCTACGTGGAGGATCTCTCTG1APPCCYGG1nValileValHisLygTxpG1uThrHisLeuG1nProArgSerIleThr	TTGGGAAACCCATTTCAAGCCCAGGTCCCTGGGA	CCCTGTACGGAGCTACAGTGCAGCTGTTGGACGTTTTCGGTATTACGTCGGACACTCC CCCTGTACGGAGCTACAGTGCAGCCAGTTGGACGTCTTCGGTATTACGTCGGACACTCC CCTGTACGGAGCTACAGAGAGAGAGAGAGAGAGAGAGAGA		rccacgacatcgagaccitigac uargleuhisTyrserGlulysProPro ::::::	CCCCAGCACGTCCAGCTGAAGATTGTGCCCGTGGAGAAGACGCTGGGCTGGCT		GAĞTGCCCTACACCAAGGGĞACATTĞTCATCTTTCACATCACGCTGCCGCTGGAG ABNSerLeuGlulleSerLeulleSerAspAsnGluPheLysCysArgHisSerGlnPro	AGGATGATGGAGGlucysGlyTyrGlyLeuGlnProA	GAGTGC	: : :	GINGLYASPATALEUPTOCIVATED THE TACK THE TEST OF THE TES	Gluseigly by sectional for the fill fill fill fill fill fill fill fil	LysThrileGlybysvalargyvalasbyyillellellystrichystricollystric		ThrileAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAspVal	

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CysThrMetValArgGlnLysGl 516
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CAGGTGATCCAGAAGGGCTGTGG 1256
                           ulleProValLysGluLeuThr 401
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CGTGCTGATCAAAGAC 1526
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|CCAAGTCACTGGGCATTGATGT 1370
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rgctacGatcGcagrgatctcrr 896
TTTCGGACTGCGAACTGCTCCG 1586
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cgagcccaggaTggaacaccgc 1430
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GACGATTGCAACTCCAAGGAGCG 956
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                                                                                                                                                                                                                   roGluAspValGlyPheAsnIl 456
                                                                                         rajareurysserbysasparg 421
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17.79E; DNA	484 pileileLeuLysThrValLeuGluAsnSerGlyLysArgArgIleValPheSerSerPh	316 CAAGGTGATCCATCAGGTGATCCAGAAGGCTGTGGCAGACCGATAATCTTCTCCAGCTT 504 eAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrProileLeuPheLe [:::	235 Qy 544 Cy 544 Db 136	CAG 11	ACTICACGCTGCCG 1055 Qy 582 ePheCysTrpGlyAsp 587	27 29	O 41	310 ; FILE REFERENCE: 10715 ; CURRENT APPLICATION : CURRENT FILING DATE: ; PRIOR APPLICATION NUM	329 764	349	369 Alignment Scores: 6.2e-45 Length:	Score: 462.00 Percent Similarity: 44.40% Best Local Similarity: 28.08% S87 Query Match: 13.06%	409 Gaps: 409 US-10-047-855-3 (1-672) x US-09-248-796A-1858 (1-2421) 527	AGIGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	
	melanogast	5.04e-52 Length: 516.00 Matches: 51.72% Conservative: 34.24% Mismatches: 14.59% Indels: 4 Gaps:	(1-672) x US-09-270-767-27552 (1-1180) luTyrSerlleGlnThrMetGluProAspAsnLeuGluLeull										390 ValGluLeuPheGluIleProValLysGluLeuThrPheAspGlnI ::: ::: 586 GACCAGCTGCAGTACCTGATCAAAAACATAAAACTTATAACTTATAAGTATAG	ABOSETPHESETGluAshGluProPh	クメラー タスト かいかんない なんない ないかい ないかい かいかい かいかい かいかい かい

243		5)
	valGlnGlyAspAlaLeuProGlyHisValGlyThrAla 255 :: ::	qq	
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1183	 GCGTTACTTAAAGATGCATACACCAAAGTAGGACCAAATTTGCGCTCATTAAATAATAGC	ò	585 Trp
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292		À 8	2329 GCT
1303	TACTTGCAAGTCTTACCTTTCAAACACAAAGCTATGAGTATTGCTAGAAGCGALACA TYTTTGLY8ProArgIleProLeuAspValGlyHisArgGlyAlaGlyAsnSerThr TYTTTGLY8ProArgIleProLeuAspValGlyHisArgGlyAlaGlyAsnSerThr TYTTTGLY8ProArgIleProLeuAspValGlyHisArgGlyAlaGlyAsnSerThr	RESULT 4 US-09-32 ; Sequen	8-352-138 ce 1388,
1360	TACTIGGAACAGCTTGTCCCACTAGAGTATCGGTCATGGTTTAGGTAAAAACTTG 1419 TACTIGGAACAGCTTGTCCCACTAGAGTATCGGTCATGGTTTAGGTAAAAACTTG 1419	; Patent; GENERJ; APPL	NO. 6563 AL INFORMI CANT: Gar
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351	SerHisGlyAlaAlaPheValGluPheAspValHisLeuSerLysAspPheValProVal 370	CURRENT APPLIC CURRENT FILINC NUMBER OF SEQ	SNT APPLI SNT FILIN SR OF SEQ
Oy 371	ValTyrHisAspLeuThrCysCysLeuThrMetLysLysPysPheAspAlaAspProVal 390 ArmmanCanGarmCaCrGTTGCAGAGTCTGGG	TYP	; CENGTH: 1161 ; TYPE: DNA ; ORGANISM: ACI
	GluLeuPheGluIleProValLysGluLeuThrPheAspGlnLeuGln	Alignme	OS-09-328-332-13 Alignment Scores
Db 1573		Score: Percent	Score: Percent Similari
Uy 40,	CCCACAGAAAACCCACTCATACAGTTGATGACG	Best Local S Query Match: DB:	cal Simil atch:
422	LysGluSerValValGlnGluGluAsnSerPheSerGluAsn	US-10-0	US-10-047-855-3
Db 1687	GCTCAATCATCGTATCAATTGTCAAATAATCACAATGACGATATTGAGAAAGAGTTTGCT 17	ζÓ	311 Ly
	15	ପ୍ର	
-	AATCAAAGGGAIGAAAGAAIGAAAIGAAAIGAAAIGAAAGAAIGAAAAGAAAIGAAAAAA	ò	331 Th
Qy 436	**************************************	අ <u>ධ</u> -	
		& A	351 Se 202 GA
-	 TACCAAATAATGTTGGTTTCAACATAGAAGTGAAATATCCTATGTTGGATGAAGCTCAA	8	
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Db 20,		δ	420 AE

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62958
MATION:
Breton et al.
Bary L. Breton et al.
Bary L. Breton et al.
FUNCTION: BUCKEIC ACID AMD AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FENTION: NUCLEIC ACID AND THERAPEUTICS
ICE: GTC99-03PA
ICATION NUMBER: US/09/328,352
IMC DATE: 1999-06-04
IQ ID NOS: 8252
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                                    350
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scccgccatgaaaatgaaattggggaacaaccaatgfaagcactttaagtcagtttgca 321
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, Application US/09328352
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Query Match: 4.33* Indels: 68 DB: 4.33* Gaps: 9 US-10-047-855-3 (1-672) x US-09-328-352-1148 (1-720) Qy 321 ValGlyHisArgGlyAlaGlyAsnSerThrThrThrAlaGlnLeuAlaLysValGlnGlu 340 Qy 321 ValGlyHisArgGlyAlaGlyAsnSerThrThrThrAlaGlnLeuAlaLysValGlnGlu 340 :::	Qy 341 AsnThrlleAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAsp 360	Oy 361 ValHisLeuSerLyshapPheValProValValTyrHisAspLeuThrCysCysLeuThr 380 :::	381 MetLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeu	Qy 401 ThrPheAspGlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAsp 420 ::: Db 220 TCATTTGATCATCGT234	Qy 421 ArgLysGluSerValValGlnGluAsnSerPheSerGluAsnGlnProPheProSer 440	441 LeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrp 	Qy 461 IleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsn 480 ::: Db 337 GTAAGAGATATGGCA 351	Qy 481 LeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgArgIleVal 500	Qy 501PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyr 519	520 ProlleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArg 	Qy 540 SerArgThrThrProllealaMetSerPhealaGlnPheGludanLeuuGud]yIle 558
418 GAACGTATTCCTGAGTTTCGACCAACACAGCTTATAATGACCTTTACCCTGTCCCA 4 440 SerLeulysMetValleuGluSerLeuProGluAsp	Db 538 GGTTTATATATTGAGACGAAACAT	491 LeuGluAenSerGlyLysArgarglleValPheSerSerPheAep 619 GCCAAATATACACGTGATATHGCACGTGTGTATTTACAGTCTTTTGAGTTCAG		Qy 509 CysThrMetValArgGlnLysGlnAsnLysTyrProlleLeuPheLeuThrGlnGlyLys 528 1		549 PhealadInPhedluAsnLeudlyIleasnValHisThr	Qy 563 GluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeuValIle 582 ::: :::::::::	Oy 583 PheCysTrpGlyAspAspThrAsnAspAroGluAsnArg 595	596Arglyschuleu 1019 PGP STANDARD CONTRARY CON	602GlyValAsnGlyLeuIleTyrAsp 609 1072 TATTTCAAGGCAGGTGTTGATGGCGTTTACGAT 1107	1148 18, Application US/09328352 5562958 Gary L. Breton et al. Gary L. Breton et al. VVENTION: NUCLEIC ACID AND AMINO ACID VVENTION: BAUMANNII FOR DIAGNOSTICS AN ENCE. GTC99-03PA PLICATION NUMBER: US/09/328,352 PLICATION NUMBER: US/09/328,352 ELING DATE: 1999-06-04 SEQ ID NOS: 8252 Acinetobacter baumannii -1148 ces: 2.22e-08 Length: 153.00 Matches: arity: 37.11% Conservative minarity: 23.02% Mismatches:

, APPLI(APPLICANT: Wiegand, Roger C.	අු	 5417 CCATGAC
FILE 1	0	δ	392 uPheGluIlePr
, CURREL	T FILING DATE: 2001-07-10 APPLICATION NUMBER: 60/217,883	QQ	5457CC
, PRIOR ; NUMBEL	PRIOR FILING DATE: 2000-07-10 , NUMBER OF SEQ ID NOS: 16825	δ	411 rHisValThrAl
SEQ ID	NO 1012 FH: 14570	qu	5507 ccacrrcacec
, TYPE	TYPE: DNA ORGANISM: Myxococcus xanthus	λ	431 rPheSerGluAs
06-60-SD	ÚS-09-902-540-1012	g	5532AC
Alignmen Pred. No	Length:	ò	444 lLeuGluSerLe
Score:	145.00 Matches: y: 33.64% Conservative:	đ	5582 GCTGCGCGCCTT
Best Local (Query Match	Similarity: 20.70% : 4.10%	λõ	464 nArgAspGlyMe
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ò		us-09	US-09-543-681A-2048 ; Sequence 2048, Applicat
q	CGCTA	, GEN	ERAL INFORMATION:
ζò	352 gGlyAlaAlaPheValGluPheAspValHisLeuSerLysAspPheValProValVaTY 372	A LIT	HITLE OF INVENTION: DU
a a		: E t	FILE REFERENCE: 2709.1
ò	372 rHisAspLeuThrCysCysLeuThrMetLysLysPheAspAlaAspProValGlube 592	-	

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À	392 uPheGlulleProValLysGluLeuThrPheAspGlnLeuGlnLeuLeuLysLeuTh 411	
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а	6035 CCCTCGAAGCCGGGATAAGCCCCGGATTCATGCCTCGCACCGCTCGCACG 6088	89
ò	647 g 647	
qq	6089 C 6089	
RESULT US-09-5 ; Seque ; Pater; ; GENEF; ; APPI; ; TITI; ; TITI; ; CURF;	RESULT 7 US-09-543-681A-2048 i Sequence 2048, Application US/09543681A i Patent No. 6605709 i APPLICANT: GARY BRETON i TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS i TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS i TITLE OF INVENTION UNMBER: US/09/543,681A CURRENT APPLICATION NUMBER: US/09/543,681A	PROTEUS MIRABIL

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Sequence 4403, Application US/09949016

Sequence 4403, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, U. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-0-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASISEQ for Windows Version 4.0
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                                                                                     576 LysAlaLysGlyLeuValllePheCysTrpGlyAspAspThrAsnAspProGluAsnArg
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Query Match:
                        CATTGT ---
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US-09-949-016-4403
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LENGTH: 1487
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ORGANISM: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 AGTTCACTTTATCAAGGGGAAAAA-----------ATTCCCACACTAAGA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --------ACATGGCCTGATGATGATGTAGAGGGC------TTATGT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345 SerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAspValHisLeuSer 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheAspAlaAspProValGluLeuPheGluIleProValLysGluLeuThrPheAspGln 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArgLys 422
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                                                                                                                                                                                                                                                                                                                                                                                               305 MetLysSerSerPheSerLysTyrTrpLysProArglleProLeuAspValGlyHisArg 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325 GlyAlaGlyAsnSerThrThrThrAlaGlnLeuAlaLysValGlnGluAsnThrIleAla 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365 LysaspPhevalProvalValTyrHisaspLeuThrCysCysLeuThrMetLysLysLys 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443 MetValLeuGluSerLeuProGluAsp---ValGlyPheAsnIleGluIleLysTrpIle 461
                                                                                                                                                                                                                                                                                                                                                                                                                                        63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 GGTGCGGTGCGCTTTCATAGTTTGATGATTACACCGTCTTGATGCAGCAGTTGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 CAAGGTTTGCAGTTGATAAAGCGCTCAGGCACTAAAGCTCAATATCGAACTTAAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      462 CysGlnGlnArgAspGlyMetTrp---AspGlyAsnLeuSerThrTyrPheAspMetAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgArgIleVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          521 IleLeuPheLeuThrGlnGlyLy8SerGluIleTyrProGluLeuMetAspLeuArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----CGTCGAGGACAGCTATGGGATGATATTCCTGATAATGCACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      561 HisThrGluAspLeuLeuArgAsnProSerTyrIle-----GlnGluAla-----
                                                                                                                                                                                                                                                                                                                                                                                                                                    13 ATGGCGATATCAACGAATAAGGAGAAGATGAAATA-----GCCGCTCATAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GTTAATCGTTGCACGAATGGACAA
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Mismatches:
Indels:
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                                                                                                                                                                                                                      Length:
Matches:
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
LENGTH: 759
                                                                                                                                                                                                      2.43e-06
136.50
39.33*
23.17*
                                                                                                                                    , ORGANISM: Proteus mirabilis US-09-543-681A-2048
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Best Local Similarity:
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EARLIER EARLIER EARLIER EARLIER NUMBER SOFTWARE SEQ ID N EDOTTA		; LOCATI US-09-247- Alignment Pred. No. Score: Percent S: Percent S: Percent G: Percent G: Percent G: Percent G: US-10-047-	8 8 8 8 8 8	8686	8 8 8 8 8 8 8
ysLeuThrMetLysLy ::: :: AACACTAGATAG ysGluLeuThrPheAs ::: :: GTGATTTGACATTTGA	TAGGAAGCTGAATCCTGCAGCAAACCACAGACTC 1ValGlnGluGluAenSerPheSerGluAenGlr 11::::- 1	-AsnLeuPheLeuAspIleIleLeuLysThrValLe :::::all ::::all ::::adAAATGTATATATATATATATATATATATATATATATATA		568 nProSerTyrIleGlnGluAlaLysAlaLysGlyLeuValIlePheCyeTrpGlyAspas 588 ::: ::::::::	RESULT 9 US-09-247-155-71 Sequence 71, Application US/09247155A Patent No. 6312922 GENERAL INFORMATION: APPLICANT: Dumas Milne Edwards, Jean-Baptiste APPLICANT: Dumas Milne Edwards, Jean-Baptiste TITLE OF INVENTION: Complementary DNAs TITLE REFERENCE: GENSET.021A CURRENT APPLICATION NUMBER: US/09/247,155A CURRENT FILING DATE: 1999-02-09 EARLIER APPLICATION NUMBER: 60/074,121 EARLIER PILING DATE: 1998-02-09 EARLIER PILING DATE: 1998-02-09 EARLIER PILING DATE: 1998-02-09 EARLIER PILING DATE: 1998-02-09 EARLIER PILING DATE: 1998-02-09
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383 sLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeuThrPheAs 403
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501 GACGACTGATGGGACTGGG------CGATTGTGTGATTTGACATTTGA 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 ------TTCGTTCTACTGCGCGTCTTCAGC------ 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sargGlyalaGlyAsnSerThrThrThrAlaGlnLeuAlaLysValGlnGluAsnThrIl 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 eAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAspValHisLe 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 uSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThrMetLysLy 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            453 TACTTCTGACGGGATTCCTGTCTTAATGCACGAT------AACACAGAGTAGATAG 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 uSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsnSerArgLysTh 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 rIleGlyLysValArgValAspTyrIleIleIleLysProLeuProGlyTyrSerCysAs 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 pMetLysSerSerPheSerLysTyrTrpLysProArg1leProLeuAsp---ValGlyHi
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82
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Matches:
Conservative:
Mismatches:
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LER APPLICATION NUMBER: 60/096,116
LIER FILING DATE: 1998-08-10
LIER APPLICATION NUMBER: 60/099,273
LIER PILING DATE: 1998-10-04
SER OF SEQ ID NOS: 182
WARE: Patent.pm
ID NO 71
                                                                                                                                                                                                                                               INFORMATION: Von Heijne matrix
INFORMATION: SCORE 10
INFORMATION: SEQ LVLLLVTRSPVNA/CL
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131.50
36.95%
21.19%
3.72%
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FION: 1590..1595
JRE:
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| KEY: sig_peptide
| ION: 148..240
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KION: 1614..1629
7-155-71
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itch:
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ION: 148..1140
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                                                                                                                               DNA
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6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6

TELECOMMUNICATION INFORMATION: TELEPHONE: (510)814-2974 TELEFAX: (510)814-2977 TELEFAX: (510)814-2977 NPORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 2682 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) 9-105-697-9	Pred. No.: 0.000203 Length: 2682 Score: 128.50 Marches: 140 Percent Similarity: 31.91% Conservative: 69 Best Local Similarity: 21.37% Mismatches: 195 Query Match: 3.63% Indels: 251 DB: 3 ** **OS******************************	150 379 170	427 AAAGACTTTACCAGCTCCTTTCCGACGCTCCACGTCCTCCACCCCGAGGGG 184 AsnSerLeuGlulleSerLeuIleSerAspAsnGluPheLysCysArgHisSerGlnPro ::: ::: ::: 481 TACCTCATCACCCCGGCCTGGCTTTGGGAAAAG	Oy 204 GlucyBolryrGlyLoughBroghtphrGlllyrsefileGininfMet 222 :: :: ::	Qy 236	Qy 273ThrLeuProlleMetSerArgAsnSerArgLysThrIleGlyLys 287 Db 796 TACGACAGAGAAACTCTTACCACTTTTGAAAGAACTGGAATTCGCATCCATC	Qy 299
423 uSerValValGluGluAsnSerPheSerGluAsnGlnProPheProSerLeuLysMe 443	684 ACACAAGGCTACTGAGGCTCTAAAGAAATGTATATGGAATTTCCTCAACTGTATAATAA 743 493 nSerGlyLysArgArg1leValPheSerSerPhe	ACAAACAGATCGGGATGTAATAACAGCATTAACTCACAGACCTTGGAGCCTAAG uPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSerArgTh CCATACAGGAGATGGGAAACCACGTTGGAGAAACCA	542 rThrProlleAlaMetSerPheAlaGluAbnLeuLeuGly1leAsnValHisTh 562	INICITOTOS INCLIGIOS CONTINUES CONTINUES CANADAS CANADAS CANADAS CONTINUES C	SSULT 10 1-09-105-697-9 Sequence 9, Application US/09105697 Sequence 9, Application US/09105697 Sequence 9, Application US/09105697 Septent No. 6228628 GENERAL INFORMATION: APPLICANT: Reichert, Fred L. TITLE OF INVENTION: MITANT CHIMERIC DNA POLYMERASE NUMBER OF SEQUENCES: 11	CORRESTONDEDS: STREET: 1080 U.S. Highway 202 STREET: 1080 U.S. Highway 202 STATE: New Jersey COUNTRY: United States ZIP: 08876 CONTRY: TRADABLE FORM:	MEDIUM TYEE: FLODEY OALS COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/105,697 FILING DATE: CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: Petry Ph.D., Douglas A. REGISTRATION NUMBER: 35321 REFERENCE/DOCKET NUMBER: 1043

	1	122
ò	332 ThralaGlnLeuAlaLysValGlnGluAsnThrIleAlaSerLeuArgAsnAlaAlaSer 351	Db 2044 C
q	1090 AAAGAGGITCIGAAAAAGCICAAAGAAAIICIGGAGGAC 1128	Qy 604 A
ò	352 HisGlyAlaAlaPheValGluPheAspValHisGeuSerLys 365	Db 2104 C
q	1129 CCCGGAGCAAAGATCGTTGGTCAGAATTTGAAATTCGATTACAAGGTGTTGATGGTGAAG 1188	RESULT 11
ò	366 AspPheValproValValTyrHisAspLeuThrCysCysLeuThrMetLysLysLys 384	252-99: ence 1
q	1189 GGTGTTGAACCTGTTCCTCCTTACTTCGACACGATGATAGCGGCT 1233	; Patent No. 65 ; GENERAL INFOR
È	385 PheAspAlaAspProValGluLeuPheGluIleProValLysGluLeuThrPheAspGln 404	
qq	1234 TACCTTCTTGAGCCGAACGAAAAGAAGTTCAATCTGGACGAT 1275	
λΌ	405 LeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArglysGluSer 424	; CURRENT APPL ; CURRENT FILI
qq	1276 CTCGCATTGAAATTCTTGGATACAAATGAGA 1308	
ò	425 ValValGlnGluGluAsnSerPheSerGluAsnGlnProPheProSerLeuLysMetVal 444	
q	1309 TCTTACCAAGAGCTCATGTCCTTCTCTTTCCGCTGTTTGGTTTCAGT 1356	; NUMBER OF SE ; SEQ ID NO 190
ò	445 LeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrpIleCysGlnGln 464	; LENGTH: 117; TYPE: DNA
QQ	1357 TTTGCCGATGTTCCTGTAGAAAAGCAGCGAACTACTCCTGTGAAGAT 1404	; ORGANISM: F US-09-252-991A-
ò	465 ArgAspGlyMetTrpAspGlyAsnLeu 473	Alignment Score
ф	1405 GCAGACATCACCTACAGACTTTACAAGACCCTGAGCTTAAAACTCCACGAGGCAGALTG 1404	Score:
à		Percent Similar Best Local Simi
qq		DB:
ò	480 AsnLeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArg 497	US-10-047-855-
q	1525 AACGGTGTGTATGTGGACACAGAGTTCCTGAAGAACTCTCAGAAGAGTACGGAAAAAA 1584	Oy 244
ò	498	Db 227
qq		0y 259
ò		Db 287
qq		Qy 273
ò		Db 346
Q	1705 ACGAAACGGGAGACTATTCAACACGCATAGAAGTCCTCGAGGAACTTGCCGGTGAACAC 1764	Qy 293
δ		Db 403
qq	-	Qy 313
ઠે		Db 442
qa	TCAATCAA	Qy 333
È		Db 481
Db		Qy 353
ò	IlePheCysTrpGlyAspAsp	Db 535
qq		Qy 373
È		265 da
qa	1984 CCTCAGGATCCAAACTGGTGGATCGTCAGTGCCGACTACTCCCAAATAGAACTGAGGATC 2043	Qy 393

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-991A-1990

No. 6551795

INPORMATION:

NO. 6551795

INPORMATION:

ANT: MARC J. RUBenfield et al.

ANT: MARC J. RUBenfield et al.

ANT: MARC J. RUBENFIELD

ANT: MARC J. RUBENFIELD

AND THERAPBUTICS

OF INVENTION:

APPLICATION NUMBER: US(09/252,991A

T PILLING DATE: 1999-02-18

APPLICATION NUMBER: US 60/074,788

APPLICATION NUMBER: US 60/094,190

FILING DATE: 1998-07-18

APPLICATION NUMBER: US 60/094,190

FILING DATE: 1998-07-27

OF SEQ ID NOS: 33142

NO 1900
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---GGAGCCACAGTGACTCTATGGACATCGCGGCGCC--------
------GluasnargarglysLeuLysGluLeuGly-----Val
                                                                                 AsnGlyLeulleTyrAspArgileTyrAspTrpMetProGluGln 618
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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4-1900
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126.50
36.55%
22.72%
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us-10-047-855-3.rni

Best Local Similarity: 23.49% Mismatches: 108 Query Match: 3.51% Indels: 80 A	Oy 341 ABNThrIleAlaSerLeuArgAshAlaAlaSerHisGlyAlaAlaPheValGluPheAsp 360	381 MetLysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeu :::::::	Db 220GTFCGCCTCACCCGTGGTGGAAGCTCCAGCGGGGGAC 258 Qy 421 ArgLysGluSerValValGlnGluGluAenSerPheSerGluAsnGlnProPheProSer 440		Db 388GAGCAGGTGGCGGGCTGGTGGCGGGGGCGGGCCGGTCGTC 438 Qy 501 PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrPro 520	Qy 521 IleLeuPheLeuThrGlnGlyLyBSerGluIleTyrProGluLeuMetAspLeuArgSer 540 ::: :::	Oy 541 ArgThr	Qy 553 GluAsnLeuLeuGlylleAsnValHisThrGluAspLeuLeuArgAsnProSerTyr1le 572	Qy 573 GlnGlualaLysAlaLysGlyLeuValllePheCysTrpGlyAspAspThrAsnAspPro 592	Qy 593 GludanargargLyaLeuLyaGluLeuGlyValasnGlyLeuIleTyrasparg 610 :::	RESULT 13 US-09-134-001C-1707 ; Sequence 1707, Application US/09134001C ; Patent No. 6380370 ; GENERAL INFORMATION: ; APPLICANT: Lynn Doucette-Stamm et al ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
	Db 700 GTACGGCCGACGCGGGCTGGAGGAGTTGTTCGAGAAGTGCCCGTTCGAG 756 Qy 453 GlyPheAsnileGluIleLysTrpIleCysGlnGlnArgAspGlyMetTrpAspGlyAsn 472 ::: ::: ::: Db 757 CACTGGCAAGTGAAGAGCGCCTCGCGCGACGCGCGGACGGA	B B B B B B B B B B	Db 868 AGCGGTTCGCGGACCGTGCTCAAGGCCCTCAACGACTGACC 909 Qy 533 ProGluLeuMetAmpLeuArgSerargThrThrProIleAlaMetSer 548	Oy 567 ArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeuValllePheCysTrpGly 586 1012 TGCACCCCGGAACGCCTGCTCAAGGCCCAGGGGCTTCACGTTCACGTCTCGGTGTGG 1068 Oy 587 AspAspThrAsnAspProGluAsnArgArgLysLeuLysGluLeuGlyValAsnGlyLeu 606	1069	DD 1126 ATCACAGAC 1134 RESULT 12 US-09-902-540-4278 : Sequence 4278, Application US/09902540	<pre>; Patent No. 6833447 ; GENERAL INFORMATION:</pre>		; FILE REFERENCE: 38-10.15349, 15.00.00.00.00.00.00.00.00.00.00.00.00.00	; NUMBER OF SEQ ID NOS: 16825 ; SEQ ID NO 4278 ; LENGTH: 762 ; TENGTH: 762	/ ORGANISM: Myxococcus xanthus US-09-902-540-4278 Alignment Scores: Pred. No.: 8.03e-05 Length: 762 Score: 124.00 Matches: 70 Percent Similarity: 36.91% Conservative: 40

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US-09-902-540-1212/c
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                                                                                                                                                                                                                                                                                                           GlyHisArgGlyAlaGlyAsnSerThrThrThrAlaGlnLeuAlaLysValGlnGluAsn
                                                                                                                                                                                                                                                                                                                                    43 GGACATAGAGGATTACCT-------AGTAAAGCTCCGGAAAAT
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TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR PLILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR PLILING DATE: 1997-08-14
SEQ ID NOS: 5674
SEQ ID NO 1707
LENGTH: 771
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74
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Indels:
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Query Match:
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US-09-134-001C-1707
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Pred. No.:
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                            687
  572
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APPLICANT: Gldman, Gregory J.
APPLICANT: Gldman, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wispand, ROGER C.
TITLE OP INVENTION: Wyxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
FILE REFERENCE: 38-10(15849)B
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
FRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1212
LENGTH 26012
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                                                                                                                        634 AAAATGGTAAAAGAAGCGGGTTATGAATTGAACGTATGG-----ACTGTAAACAAACCA
GluAsnLeuLeuGlyIleAsnValHisThrGluAspLeuLeuArgAsnProSerTyrIle
                                                                                  573 GlnGluAlaLysAlaLysGlyLeuValIlePheCysTrpGlyAspAspThrAsnAspPro
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                                                                                                                                                                                           688 GCACGIGCAAACTIGCIAATIGGGAGTIGAIGGIAICTITACAGAC 738
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                                                                                                                                                                                                                                                                                                    Sequence 1212, Application US/09902540 patent No. 6833447; GENERAL INFORMATION:
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Alignment Scores: 0.00216 Length: 3393 Pred. No.: 121.50 Matches: 162 Score: 33.62\$ Conservative: 108 Best Local Similarity: 20.17\$ Mismatches: 291 Query Match: 3.44\$ Indels: 243 DB: 3 44\$ Gaps: 41 US-10-047-855-3 (1-672) x US-09-104-324B-1 (1-3393)	22 IleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeuLeu:::	Qy 42 ProGluAsnAspThrGlyGuserMetLeuTrp 52	Qy 53 LysalaThrIleValLeuSerArgGlyValSerValGlnTyrArgTyrPheLysGlyTyr 72	Qy 73 PheLeuGluProLysThrIleGlyGlyProCysGln-Va 85	Qy 85 111eValHisLysTrpGluThrHisLeuGlnProArgSerlleThrProLeuGluSerGl 105	105 ullellelledapasp 105 ullellelledapasp 106 ullellelledapasp 107 ullellelledapasp 108 ullellelledapasp 108 ullellelledapasp 108 ullellellellellellellellellellellellelle
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817 TAAGTTAAAGGAAGATTATGAAAAAATCCAACACCTTGAACAAGAATACAAGGAAAT 876 248 uProglyhisValGlyThralaCysLeucserSerThrIlealaGluSerGlyLysSe 268	
TGCTAGAGGAATCCAGAGATAAAGTTAATCAATTAGAGGA	
275ProllemetSerargasnSerargLysThrIleGlyLysValargValaspTy 292 :::	
292 rIleIleIleLysProLeuProGlyTyrSerCysAspMetLysSerSerPheSerLysTy 312 ::::	
312 rTrpLysProArg11eProLeuAspValG1yHisArgG1yAlaG1yAsnSerThrThrTh 332 ::: 1108 AAAGGCTTTAGAGGAAGATTTACAGATAGCAACAAAAACAAT 1149	
332 ralaGinLeualaLysValGinGluAsnThrIlealaSerLeuArgAsnAlaAlaSe 351 :: :: :: 1150 TTGTCAGCTAACTGAAGAAAAACTCAAATGGAAGAATCTAATAAAGCTAGAGCTGC 1209	
351 rHigGlyAlaAlaPheValGluPheAspValHisLeuSerLysAspPheValProValVa 371 	
371 lTyrHisAspLeuThrCysCysLeuThrMetLysLysLysPheAspAlaAspProValGl 391 	
391 uleuPheGluIleProValLysGluLeuThrPheAsp	
405 uGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArgLysGluSe 424 ::::::	<u> </u>
424 rValValGlnGluGluAsnSerPheSerGluAsnGlnProPheProSerLeuLysMetVa 444 ::: :::::	
464 nargaspglymetTrpaspglyasnLeuSerThrTyrPheAspMetAsnLeuPheLeuAs 484	
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511 tValargGlnLysGlnAsnLysTyrProlleLeuPheLeuThrGlnGlyLysSerGlull 531 ::::::	
531 eTyrProGluLeuMetAspLeuArgSerArgThrThrProlleAlaMe 547	
547 tSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnValHisThrGluAspLeuLeuAr 567	

567 gABNProSertyrileGinglualaLysalalysGlyLeuValilePheCysTr 585	585 pGlyaspaspThrasnasp	597 sLeuLysGluLeuGlyValAsnGlyLeuIleTyrAspArglleTyrAspTrpMetPr 616 :::::: 1933 GTATATTGAAGAACTTCAGCAGGAGAATAAGGCCTTGAAAAAAAA	616 oGluGlnProAsnIlePheGlnValGluGlnLeuGluArgLe 630 :::	630 uLysGlnGluLeuProGluLeuLysSerCysLeuCysProThrValSerArgFheValPr 650 ::: 2053 CAAACAGAAATTTGGAGAAATCACAGAGCACCTATCAGAAGAAATTGA 2100	OSerSerLeuCysGlyGluSerAspIleHisValAspAlaAsnGlyIleAspAsnValGl 670	
GASNProSerTyrIle- AAATGAACTAGAATATGTGA	pGlyaspaspThrasnasp- artggacaagagtgaagaaa	sLeulysGluLeuGly ^v :::::: GTATATTGAAGAACTTCAGC	ogluglnProAsnIlePhed -:: CAAGCACTGAATGTTTATG	uLysGlnGluLeuProGluI :: CAAACAGAAATTTGGAGAAA	650 oSerSerLeuCysGlyGluSerAspIleHi ::::: 2101 GGACAAAAGATATCAGAAGAAATCTT	670 uAsnAla 672 2143 GAAAGCA 2149
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bone marrow; leukaemia; platelet; thrombocytopenia; thrombosis; B-cell;
T-cells; neutropenia; gene therapy; human; ss; gene; Narcl6b.
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/product= "Human Narc16b (64549) protein"
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AbJ57938
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-USB-N Geneseq_16Dec04 -QFMT=fastap -SUDFIX=rng -MINMATCH=0.1 -LGOPCL=0
-LGOPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-USBR=US10047855_@CGN_1 1_644_@runat_01072005_155528_2208 -NCPU=6 -ICPU=3
-NOMBL-LARGEQUERY -NGG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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26-AUG-2003; 2003US-0498106P.
15-SEP-2003; 2003US-0500179P.
16-SEP-2003; 2003US-0502909P.
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AAD06010 standard; DNA; 3206 BP AAD06010

AAD06010;

(first entry) 31-JUL-2001 Human neuronal apoptosis regulated candidate (NARC) 16B DNA.

Human; neuronal apoptosis regulated candidate 16B; NARC 16B; cytostatic; chromosome mapping; gene therapy; antisense therapy; lung disorder; central nervous system disorder; apoptosis; spleen disorder; angina; tuberculosis; Goodpasture's syndrome; liver disorder; jaundice; infectious disorder; brain disorder; cerebral oedema; gonorrhoea; heart disorder; kidney disorder; glomerulonephritis; testes; virucide; epididymis disorder; skeletal muscle disorder; pancreatic disorder; diabetes; cytoprotectant; immunostimulant; tumour; antiinflammatory; antimicrobial; neuroprotective; gynaecological; ds.

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WO200131007-A2

03-MAY-2001

20-OCT-2000; 2000WO-US029132

99US-0161188P 22-OCT-1999; (MILL-) MILLENNIUM PHARM INC

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161 LeuThrLeuGluGlyLeuGluGluAspAspAspAspArgValSerProThrValLeuHis 180

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The invention relates to human homologues of neuronal apoptosis regulated candidate (NARC) nucleic acid molecules and proteins derived from rat candidate (NARC) nucleic acid molecules and programmed cell death libraries. The nucleic acids of the invention are useful for assaying the presence of a nucleic acid molecule and for chromosome mapping. They are also used in gene therapy and antisense therapy. The NARC sequences are useful for treating central nervous system disorders and disorders involving aberrant apoptosis, for inducing an immune response and for isolating binding partners. Diseases treated include spleen disorders (e.g. tuberculosis and congestive splenomegaly), lung disorders (e.g. tuberculosis and congestive splenomegaly), lung disorders (e.g. tuberculosis and congestive splenomegaly), lung disorders (e.g. tuberculosis and congestive condpasture's syndrome, infectious disorders (e.g. viral jaundice and hydrocephalus), heart disorders (e.g. viral concephalus), heart disorders (e.g. viral magina and myocardial infarction), kidney disorders (e.g. cysts and splenomegaly), skeletal muscle disorders (e.g. tumours) and pancreatic shuman neuronal apoptosis regulated candidate (NARC) 16B DNA Rat brain polypeptides, nucleic acids and antibodies, useful for diagnosis and treatment of central nervous system disorders and disorders associated with aberrant apoptosis. Claim 1; Page 148; 161pp; English. WPI; 2001-308641/32.

Sequence 3206 BP; 988 A; 580 C; 682 G; 956 T; 0 U; 0 Other;

Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Ouery Match:	0 3537.00 100.00% 100.00%	Length: Matches: Conservative: Mismatches:	3206 672 0 .
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US-10-047-855-3 (1-672) x AAD06010 (1-3206)

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21	AlaileCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40	
205	GCGATATGTGGAAGCTGTGTGTTTGGGAAACTGGAATCCTCAAAATGCTGTGGCTCTT 264	
41	LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg 60	
265	CTTCCAGAGAATGACACAGGTGAAAGCATGCTATGGAAAGCAACCATTGTACTCAGTAGA 324	
61	GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly 80	
325	GGAGTATCAGTACGCTACTTCAAAGGGTACTTTTTAGAACCAAAGACTATCGGT 384	
81	GlyProCysGlnValileValHisLysTrpGluThrHisLeuGlnProArgSerIleThr 100	
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101	ProLeuGluSerGluIleIleIleAspAspGlyGlnPheGlyIleHisAsnGlyValGlu 120	
445	CCTTTAGAAAGCGAAATTATTATTGACGATGGACAATTTGGAATCCACAATGGTGTTGAA 504	
121	Η-	
202	ACTCTGGATTCTGGATGGCTGACATGTCAGACTGAAATAAGATTACGTTTGCATTATTCT 564	
141	GluLysProProValSerlleThrLysLysLeuLysLeuLysEysSerArgPheArgValLys 160	
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NARCIO; NARCIG; cytostatic; immunosuppressive; dermatological; cardiant; KW antiniflammatory; nephrotropic; anti-HIV; nootropic; neuroprotective; antiniflammatory; nephrotropic; anti-HIV; nootropic; neuroprotective; maintinical antimanic; hypotensive; kw antianaemic; cerebroprotective; vasotropic; antimanic; hypotensive; kw immunosuppressive; thyromimetic; jammunostimanic; hypotensive; tranquiliser; neuroleptic; gene therapy; gene mapping; apoptosis; kw tranquiliser; neuroleptic; gene therapy; gene mapping; apoptosis; kw viral infection; nucleosome assembly; phosphate homeostasis; kw viral infection; cancer: follicular lymphoma; carcinoma; call cycle regulation; cancer: follicular lymphoma; carcinoma; kw p53 mutation; graft rejection; hormone-dependent tumour; kw systemic lupus erythematosus; diabease; hashimoto's thyroiditis; kw systemic lupus erythematosus; diabease; hashimoto's thyroiditis; kw acquired immunodeficiency syndrome; neurodegenerative disease; etroke; kw holzheimer's disease; parkinson's disease; carebellar degeneration; kw myelodysplastic syndrome; ischaemic injury; nyocardial infarction; kw reperfusion injury; liver disease; didopathic dilated cardiomyopathy; kw myelodysplastic syndrome; ischaemic injury; nyocardial infarction; kw myelodysplastic syndrome; ischaemic injury; nyocardial infarction; my myelodysplastic syndrome; ischaemic injury; nyocardial infarction; kw myelodysplastic syndrome; order sunstery; my myelodysplastic syndrome; order sunstery; my myelodysplastic syndrome; cardiomyopathy; aplastic anaemia; chronic neutropaenia; mania; kw myelodysplastic syndrome; order sunstery;
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16-JAN-2001; 2001US-0262306P. 16-JAN-2002; 2002WO-US001098 (MILL-) MILLENNIUM PHARM INC

WPI; 2003-058503/05.

P-PSDB; ABB84606.

Novel isolated programmed cell death-related polypeptide, NARC10 and NARC16, useful for treating disorders associated with abnormal apoptotic process e.g. Alzheimer's disease, cancer, myocardial infarction, stroke.

Claim 1; Fig 4A-C; 123pp; English

munications are actual control of the manical manufactory. Cerestropic, neuroprotective, antidabetic, immunosuppressive, cytostatic; thyromimetic, nephrotropic, controlic, neuroprotective, antidabetic, immunosuppressive, cytostatic; thyromimetic, nephrotropic, controlic, immunosuppressive, cytostatic; thyromimetic, nephrotropic, immunostimulant, anticonvulsant, tranquiliser, hypotensive and can be used in gene therapy. The products of the invention can be used to modulate NARCHO or NARCHO polyucleotides, to map NARC genes on a chromosome, e.g. to locate gene conjour associated with genetic disease or to associate NARCHO or NARCHO cypolyucleotides, and are therefore useful for modulating the apoptoric process, and are therefore useful for modulating and treating disorders associated with increased apoptosis, inhibition of apoptosis or distruptions in cell cycle. For regulating cellular functions including process, and are therefore useful for modulating, and treating disorders associated with abnormally, phosphate homeostasis and the creating disorders associated with abnormally low rate or abnormally high crate of apoptosis e.g. cancers including follicular lymphomas, carcinomas with p53 mutations, or hormone-dependent tumours, autoimmune disorders including systemic lupus expthematosus, diabetes, graft rejection, including acquired immunodeficiency syndrome (Including Alzheimer's disease, Parkinson's disease, controled of pigmentosa, and cerebellar degeneration), myelodysplastic syndromes (Including Alzheimer's disease, parkinson's disease, chronic cardiomyopathy and valvular heart disease, paparatic syndromes (including Alzheimer's disease, paparatic syndromes (including Alzheimer's disease, paparatic syndromes (including Alzheimer's disease, paparatic syndromes (including Alzheimer's disease, paparatic syndromes (including Alzheimer's disease, paparatic syndromes (including alzheimer's disease, paparatic syndromes contropaenia, and myelodysplastic syndromes cardiomyopathy and valvullar heart disease, paparat This invention describes novel cell death-related polypeptides NARC10 and NARC16, located on chromosome 4q11-4q21 and which have cardiant, antiHIV, immunosuppressive, dermatological, antiinflammatory, cerebroprotective,

U; 0 Other; Sequence 3206 BP; 988 A; 580 C; 682 G; 956 T; 0

3206 672 0 0 0 Length:
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MetThrProSerGlnValAlaPheGluIleArgGlyThrLeuLeuProGlyGluValPhe

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cerebroprotective; dermatological; virucide; neuroprotective; phosphatidylglycerolphosphate synthase; PGP synthase; human;
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                   ThrPheAspGlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAsp
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The present invention provides isolated nucleic acid molecules and proteins designated 27411, 23413, 22438, 23553, 25278, 26212, NARC SC1, proteins designated 27411, 23413, 22438, 23553, 25278, 26212, NARC SC1, NARC 104, NARC 124, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 127, NARC 
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Kapeller-Libermann R, Meyers RE, Chiang LW, Hunter JJ;
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                                                                                                                          22-OCT-1999; 9908-0161188P.
31-JAN-2000; 2000US-0161188P.
28-FBB-2000; 2000US-0165517P.
20-OCT-2000; 2000US-0073426.
31-JAN-2001; 2001US-00773426.
28-FBB-2001; 2001US-00773426.
31-OCT-2001; 2001US-035503P.
31-OCT-2001; 2001US-035503P.
25-MAR-2002; 2002US-00105992.
26-AUG-2002; 2002US-0018662.
30-OCT-2002; 2002US-00284014.
30-OCT-2002; 2002US-00284014.
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30-APR-2003; 2003US-00426776.
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ון איים איים אייא אייא איים טיים טיים טייב אייא טייב איים טייב איים טייב איים אייא איים איים איים אייא איי	264 60 324 80 384 100	120 504 140 160 624 180	rghis rghis GGCaT 1eGln INCI TACAG TACAG TACAG TACAG TACAG	280 OY 280 Db 984 OY 300 Db 1044 OY 320 Db 1104 ABV29 340 ID	1164 XX 360 XX 1224 XX 1224 XX 1284 XX 400 XX 1344 PN 1344 PN

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                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                          17-FEB-2000; 2000US-0183319P.
16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-025281P.
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                         PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrPro
                                     TTTTCTTCATTTGATGCAGATATTTGCACAATGGTTCGGCAAAAAGCAGAACAAATATTCCG
                                                              IleLeuPheleuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSer
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                                                                                                  ArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnVal
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The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. noncancerus) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the conceptions ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention and a method of treating a corresponding to a marker of the invention. The patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the carpression levels indicates ovarian cancer. The level of expression of a corresponds to a secreted protein or to a transcribed marker is assessed by detecting the presence in the sample, a protein or protein cancer is assessed by detecting the presence in the sample, a protein or protein cancer is assessed by detecting the presence of polymucleotide or its portion. The level of expression of a corresponding to the marker. The presence of protein or protein cancer is assessed by detecting the presence of protein or protein fragment is detected using an antibody that specifically binds with the corresponding to the marker. The level of expression of the marker is assessed by detecting the presence of a transcribed corresponding the marker or anneals with a portion of the polymucleotide which anneals with the marker or anneals with a portion of protein is also become a farmacribed or marker is a second for morniparing the marker or anneals with a portion of protein or p cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer. marker is also used for monitoring the progression of ovarian cancer in patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the marker in a patient time and comparing the level of expression. The method at a subsequent using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer This sequence represents a human ovarian cancer DNA marker of the invention. ID NO 21000; 106pp; English. Disclosure, SEQ

Sequence 3499 BP; 1104 A; 610 C; 736 G; 1039 T; 0 U; 10 Other;

3499 672 0 0 0 Conservative: Mismatches: Indels: Gaps: Length: Matches: 100.00% 100.00% 100.00% Similarity: Percent Similarity: Query Match: DB: Best Local

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۵	221	AIGACACCTICTCAGGITGCCTTTGAAATAAGAGGAACTCTTTTACCAGGAGAAGTTTTT	280
>-	21	AlaileCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu	40
Ω	281	GCGATATGTGTGTTTTTTTTTTTTTTTTTTTTTTTTTTT	340
>-	41	LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg	09
۵	341	CTTCCAGAGAATGACACAGGTGAAAGCATGCTATGGAAAGCAACCATTGTACTCAGTGA	400
>-	61	61 GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly 8	80
. م	401	GGAGTATCAGTATCGCTACTTCAAAGGGTACTTTTTAGAACCAAAGACTATCGGT 4	460
>-	81	GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr	100
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۵	521	CTTTTAGAAAGCGAAATTATTATTGACGATGGACAATTTGGAATCCACAATGGTGTTGAA S	980

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38888 38888	the invention telates to movel polynucleorine and polypoptices for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for disploasing or treating psoriasis in a mammal. This sequence	& a	281 SerargiysThrileGlyLysValArgValAspTyrileIleIleIleLysProLeuProGly 300
S S S	equence 5443 BP; 1544 A; 1034 C; 1149 G; 1716 T; 0 U; 0 Other;	å 8	301 TyrSerCygAspMetLygSerSerPheSerLysTyrTrpLysProArg11eProLeuAsp 320
Alignment Pred. No.: Score: Percent Sin	Scores: milarity:	y da	321 ValGlyHisArgGlyAlaGlyAsnSerThrThrThrAlaGlnLeuAlaLySValGlnGlu 340
DB:	arlry: 100.00% mismacches: 100.00% Indels: 12 Gaps:	& 8	341 ASITHITIEALASELLEUALGASIALAASERHISGIYALAALAPHEVAIGIUPHEASP 360
US-10-047-85 Qy	5-3 (1-672) x ADNO5171 (1-5443) 1 MetThrProSerGlnValAlaPheGluIleArgGlyThrLeuLeuProGlyGluValPhe	δ qa	361 ValHisLeuSerLygAspPheValProValValTyrHisAspLeuThrCysCysLeuThr 380
9 & 8	205 AIGACACCITCICAGGITGCCTTIGAAAIAAGGAGGACTCTTTTACCAGGAGAAGITTTT 264 21 AlaileCysGlySerCygAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40 22 CCTAILLE THE THE THE THE THE THE THE THE THE TH	% a	381 Metlyslyslyspheaspalaaspprovalgluleupheglulleprovallysgluleu 400
3 & 8	1 LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg	ço Op	401 ThrPheAspGlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAsp 420
8 8	GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThr11eGly 	& g	421 ArgLysGluSerValValGlnGluGluGanSerPheSerGluAsnGlnProPheProSer 440
3 & 5	1 GlyProCysGlnVallleValHisLysTxpGluThrHisLeuGlnProArgSerlleThr GlyProCysGlnVallleValHisLysTxpGluThrHisLeuGlnProArgSerlleThr HIII	& g	441 LeulysMetValleuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrp 460
8 & 8	ProLeuGluSerGlulleIlelaspAspAspGlulleHishsnGlyValGlu	상 음	461 IleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsn 480
8 8 8	ThrLeuAspSerGlyTrpLeuThrCysGlnThrGlulleArgLeuArgLeuHisTyrSer 	& a	481 LeuPheLeuAspileileLeuLysThrValLeuGluAsnSerGlyLysArgArgileVal 500
ර සි	GluLysProProValSerIleThrLysLysLeuLysLysSerArgPheArgValLys 	ov G	501 PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrPro 520
8 8 8	LeuThrLeuGluGlyLeuGluGluAspAspAspAspArgValSerProThrValLeuHis	\$ a	521 IleLeupheLeuThrGlnGlyLysSerGlulleTyrProGluLeuMetAspLeuArgSer 540
8 8	1 LysMetSerAsnSerLeuGlulleSerLeulleSerAspAsnGluPheLysCysArgHis	રું વ <u>વ</u>	541 ArgThrThrProlleAlaMetSerPheAlaGlnPheGluAsnLeuLeuGly11eAsnVal 560
3 & 8	SerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGln	& g	561 HisThrGluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeu 580
ે ઠે કે	ThrMetGlubroAspAsnLeuGluLeuIlePheAspPhePheGluGluAspLeuSerGlu	Qy Qa	581 ValilepheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLysLeuLysGlu 600
3 &	1 HisvalvalGinGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSer	& 93	601 LeuGlyValasnGlyLeuIleTyraspargIleTyraspTrpMetProGluGlnProAsn 620
음 &	925 CACGTAGTTCAGGGTGATGCCCTTCCTGGACATGTGGGTACAGCTTGTCTTTATCATCC 984 261 Thr1leAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsn 280	λο 	621 IlePheGlnValGluGlnLeuGluArgLeuLysGlnGluLeuProGluLeuLysSerCys 640

2065 ATATICCAAGIGGAGCAAIIGGAACGCCIGAAGCAGGAAIIGCCAGAGCIIAAGAGCIGI 2124

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The present sequence is of cDNA clone DNA327983 encoding novel human PRO polypeptide PRO81903. The invention provides newly identified and colypeptide sequences encoding polypeptides referred to as PRO isolated diseases microarray analysis showed that DNA327983 is upcompared diseases microarray analysis showed that DNA327983 is upcompared to newless patients, up-regulated 1.3-fold in lesional skin as compared to non-lesional skin from provises patients as compared to normal colon samples from Crohn's compared to normal colon and up-regulated 1.3-fold in Colon and the blood cells from rheumatoid arthritis patients as compared to those from healthy donors. It is also down-regulated 1.5-fold upon activation of corpus with CD28 or ICAM and down-regulated 1.5-fold upon activation of monocytes with LPS. PRO8393 can be used in a claimed corpus in the compound that inhibits expression of the generator of identifying a compound that inhibits expression of the generator of identifiation compound is especially an antisense nucleic cof rheumatoid arthritis. Crohn's disease and psoriasis. A vector of rhematoid arthritis. Crohn's disease and psoriasis. A vector comprising the present nucleic acid can be used to transform a host cell, especially a CHO cell, Escherichia coli or yeast, for production of the corpus or production of the corpus or the coll or production of the corpus or coll or production of the corpus or collaboration or displaced conditions are collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collaborated collab
                           2125 TIGIGICCCACTGITAGCCGCTTIGITICCTCATCTTIGIGGGGGGGGCTGGATAICCAT 2184
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LeuCysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHis
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                                                                                                                            661 ValaspalaAsnGlyIleAspAsnValGluAsnAla 672
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/product= "PRO83903"
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P-PSDB; ADS74321.
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                                                                                                                                          21 AlaileCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu
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                                                                                                                                  LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg
Sequence 5443 BP; 1544 A; 1034 C; 1149 G; 1716 T; 0 U; 0 Other;
                    Length:
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Mismatches:
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Gaps:
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABW00010-ABW22213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer; (b) monitoring the progression of nihibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; determining whether prostate cancer has metastasized in a patient; (l) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                 cancer; cytostatic; carcinogen; pharmacodyanamic marker;
marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 ATGACACCTTCTCAGGTTGCCTTTGAAATAAGAGGAACTCTTTTACCAGGAGAAGTTTTT
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16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-020454P.
09-UTN-2000; 2000US-021314P.
18-JUL-2000; 2000US-0219007P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid molecules and polypeptides (e.g. 27411, 23413, 22438, 23553, NARC SCI or NARC 1) useful for diagnosing, preventing or treating disorders associated with the protein, e.g. cancer, atherosclerosis or AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides isolated nucleic acid molecules and proteins designated 27411, 23413, 22418, 23553, 25278, 26212, NARC S1, NARC 19, NARC 10, NARC 11, NARC 11, NARC 11, NARC 11, NARC 11, NARC 14, NARC 11, NARC 14, NARC 15, NARC 19, NARC 20, NARC 20, NARC 24, NARC 26, NARC 27, NARC 26, NARC 26, NARC 27, NARC 11, NARC 16, NARC 19, NARC 20, NARC 27, NARC 28, NARC 16, NARC 9, NARC 27, NARC 28, NARC 16, NARC 11, NARC 27, NARC 29, NARC 20, NARC 20, NARC 20, NARC 20, NARC 20, NARC 20, NARC 20, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, NARC 21, N
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drug screening; gene therapy; cytostatic; hepatotropic; nootropic; cerebroprotective; dermatological; virucide; neuroprotective; phosphatidylglycerolphosphate synthase; PGP synthase; rat; ss.
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99US-0161188P.
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Kapeller-Libermann
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                                                                             norvegicus
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Best Local Similarity:
                                                                                                                US2004009553-A1
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31-AN-2000;
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nervous system disorder; autoimmune disorder; inflammation; allergy;
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                                                                                              ProSerLeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIle
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                                  LysAspArglysGluSerValValGlnGluAsnSerPheSerGluAsnGlnProPhe
                                                                      GluLeuThrPheAspGlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSer
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                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to bone marrow expressed polynucleotides and proteins. These sequences can be used in the treatment of inflammatory conditions (eg arthritis, Crohn's disease), cancer, central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's and Huntington's diseases, spinal cord disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid cell disorders, platelet disorders, stem cell disorders, bone degenerative disorders, autoimmune disorders, for example multiple solerosis, diabetes and arthritis, viral and bacterial infections, allergies and blood coagulation disorders. The present sequence is a DNA allergies.
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                                                                                                                                                                                                                                                                       New bone marrow-expressed nucleic acids and polypeptides, useful for diagnosis, treatment of inflammatory, autoimmune, neurological, cancer and increasing hematopoiesis, stem cell survival and bone growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluValPheAlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAla
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                                                                                                                                                                                     Ford JE,
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                                         31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
30-NOV-2000; 2000US-0250583P.
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30-MAR-2001; 2001WO-US010472
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WPI; 2001-308641/32.
   WO200131007-A2
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Homo sapiens.
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20-OCT-2000; 2000WO-US029132.
                                        99US-0161188P
                                                                                 (MILL-) MILLENNIUM PHARM INC
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Rat brain polypeptides, nucleic acids and antibodies, useful for diagnosis and treatment of central nervous system disorders and disorders associated with aberrant apoptosis.

Claim 1; Page 146; 161pp; English.

The invention relates to human homologues of neuronal apoptosis regulated CC candidate (NARC) nucleic acid molecules and proteins derived from rat candidate (NARC) nucleic acid molecules and proteins derived from rat brain and programmed cell death libraries. The nucleic acids of the convention are useful for assaying the presence of a nucleic acid molecule and for chromosome mapping. They are also used in gene therapy and can tisense therapy. The NARC sequences are useful for treating central nervous system disorders and disorders involving aberrant apoptosis, for inducing an immune response and for isolating binding partners. Diseases treated include spleen disorders (e.g. tuberculosis and congestive congopasture's syndrome and bronchial asthma), liver disorders (e.g. viral congopasture's syndrome and bronchial asthma), liver disorders (e.g. viral conceptable), infectious disorders (e.g. viral conceptable), heart disorders (e.g. heart failure, encephalopathy and hydrocephalus), heart disorders (e.g. heart failure, capping and myocardial infarction), kidney disorders (e.g. carebrasione) and pancreatic syphilis), skeletal muscle disorders (e.g. tumours) and pancreatic is human contronal apoptosis regulated candidate (NARC) 98 DNA

Sequence 2738 BP; 880 A; 450 C; 540 G; 868 T; 0 U; 0 Other;

			CCGGAGTGTGGT 77	GluProAspAsn 226	schaccachinac 137	.ValGlnGlyAsp 246	Grrcaggraar 197	AlaGluSerGly 266	recreacacicca 257	JLysThrileGly 286	SAAAACAATAGGC 317
2738 486 ive: 0 s: 0		GluileSerLeuileSerAspAsnGluPheLysCysArgHisSerGlnProGluCysGly	GAGATATCCTTAATAAGCGACAATGAGTTCAAGTGCAGGCATTCACAGCCGGAGTGTGGT	TyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGlnThrMetGluProAspAsn	TATGGCTTGCAGCCTGATCGTTGGACAGAGTACAGCATACAGACGATGGAACCAGATAAC	LeuGluLeullePheAspPhePheGluGluAspLeuSerGluHisValValGlnGlyAsp	CIGGAACTAATCTTTGATTTTTTCGAAGAAGATCTCAGTGAGCACGTAGTTCAGGGTGAT	247 AlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSerThrIleAlaGluSerGly		LysSerAlaGly1leLeuThrLeuProlleMetSerArgAsnSerArgLysThr1leGly	AAGAGTGCTGGAATTCTTACTCTTCCCATCATGAGCAGAAATTCCCGGAAAACAATAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides isolated nucleic acid molecules and proteins designated 27411, 23413, 22438, 23553, 25578, 26212, NARC SC1, NARC 10A, NARC 10A, NARC 11, NARC 13, NARC 17, NARC 24, NARC 27, NARC 31, NARC 15, NARC 19, NARC 20, NARC 26, NARC 27, NARC 26, NARC 27, NARC 28, NARC 36, NARC 15, NARC 16, NARC 19, NARC 20, NARC 91, NARC 161, NARC 10C, NARC 91, NARC 27, NARC 162, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C, NARC 10C,
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glomerulonephritis, osteoporosis, AIDS (acquired immunedeficiency syndrome), Parkinson's disease, Alzheimer's disease, stroke and dermatitis. These may also be used in drug screening. The invention also useful in gene therapy. The present sequence is human neuronal apoptosis regulated candidate (NARC) cDNA.
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               AsplleCysThrMetValArgGlnLysGlnAsnLysTyrProlleLeuPheLeuThrGln
                                                                                                    GlyLysSerGluIleTyrProGluLeuMetAspLeuArgSerArgThrThrProIleAla
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         GlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsnLeuPheLeuAspIleIle
                                                      MetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnValHisThrGluAspLeuLeu
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2000US-0250583P.
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                                                                                                                                                      marrow-expressed nucleic acids and polypeptides, useful for
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Neuronal apoptosis regulated candidate; NARC; diagnosis; cancer; lung disease; cirrhosis; hepatitis; atherosclerosis; myocardial infarction; inflammation; anaemia; glomerulonephritis; osteoporosis; AIDS; acquired immunedeficiency syndrome; Parkinson's disease; Alzheimer's disease; stroke; dermatitis; drug screening; gene therapy; cytostatic; hepatotropic, nootropic, cerebroprotective; dermatological; virucide; neuroprotective; phosphatidylglycerolphosphate synthase; PGP synthase; rat; ss.
                                                                                                                                                                                                                  Rattus norvegicus,
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New isolated nucleic acid molecules and polypeptides (e.g. 27411, 23413, 25438, 23553, MRKC Scl or NARC 1) useful for diagnosing, preventing or treating disorders associated with the protein, e.g. cancer, atherosclerosis or AIDS.
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apoptosis regulated candidate (NA
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27-SEP-1999; 99US-00406045.
22-OCT-1999; 99US-0161188P.
31-JAN-2000; 2000US-016517P.
20-OCT-2000; 2000US-0185517P.
20-OCT-2000; 2001US-00592785.
31-JAN-2001; 2001US-00795691.
31-OCT-2001; 2001US-0335037P.
31-OCT-2001; 2001US-03593.
25-MAR-2002; 2002US-0025962.
26-AUG-2002; 2002US-00229662.
30-OCT-2002; 2002US-00284014.
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Kapeller-Libermann R,
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Length: Matches:

6.14e-132 1399.00

Alignment Scores: Pred. No.: Score:

ADJ57947 standard; cDNA; 2393

RESULT 15 ADJ57947 ID ADJ5

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Gaps:
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BC033408 M18 muscu

AX12755 Sequence

AX01947 Homo sapi

AX12510 Mus muscu

BD149663 Primer fo

AX869601 Sequence

AX069505 Drosophil

CO577356 Sequence

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CO577357 Drosophil

AC01993 Drosophil

AC092231 Drosophil

AC092231 Drosophil

AC092240 Drosophil

AC09231 Drosophil

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AC099654 Homo sapi
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0131007-A 4 03-MAY-2001;

Millennium Pharmaccuticals, Inc. (US)

Location/Qualifiers

1. 3206

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/mol type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 4 from Patent W00131007.
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AX817873
AX01347
AX122510
BD149563
AX069501
AX069505
CC577355
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AC092240
AC092231
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AC0402576
CQ403276
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AX127528
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-FGAPOR=17 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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27-MAR-2003 LeuPheLeuAspileileLeuLysThrValLeuGluAsnSerGlyLysArgArgleVal ArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnVal HisThrGludspLeuLeudrgdsnProSerTyrIleGlnGludlaLysAlaLysGlyLeu ValilePheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLysLeuLysGlu ThrPheaspGlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysBap PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrPro PAT linear ValAspAlaAsnGlyIleAspAsnValGluAsnAla 672 DNA 3206 bp 4 from Patent WO02081516. AX675186 Sequence NOI

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Catarrhini, Hominidae, Homo.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAK Plate: 34 Row: a Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 25901061.
Location/Qualifiers
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                                                                                         Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurac
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                            Contact: MGC help desk
Email: cgapbs-r@mail.nin.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
                                                                                                                                                                                                                    this sequence version replaced gi:20379525
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/product=hypothetical protein KIAA1434"
/protein_id="AAH37588.1"
/db_xref="GI:20379526";
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/db_xxef="LocusID:56261"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="MGC:26147 IMAGE:4827346"
/tissue_type="Testis"
/clone_lib="NIH MGC_97"
                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 25, 2003 this sequence version repla
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Altechnia, S. F., Grouse, L.H., Derge, J.G.,
Rlausherg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Rlausher, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M. B., Bonaldo, M.F., Casarant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Male, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Muzny, D.M., Sodersen, B.D., Hulyk, S.W.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, A., Rodrigues, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and mouse cDNA sequences
L. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                          CTGTTTTTGGATATAATTTTTAAAACTGTTTTAGAAATTTCTGGGAAGAGAGAATAGTG 1644
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                            PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrPro
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                                                                 TyrSerCysAspMetLysSerSerPheSerLysTyrTrpLysProArglleProLeuAsp
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                                                                                                                                 ValGlyHisArgGlyAlaGlyAsnSerThrThrThrAlaGlnLeuAlaLySValGlnGlu
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                  ThrileAlaGluSerGlyLygSerAlaGlyIleLeuThrLeuProlleMetSerArgAsn
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trapy of ovarian cancer
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Db 221 AIGACACCTICTCAGGITGCCTITGAAATAAGAGGAACTCTTTTACCAGGAGAAAGTTTTT 280 Qy 21 AlaileCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40 Db 281 GCGATATGTGGAAGCTGTGATGCTTTGGGAAACTGGAAATCCTGAAAATGCTGTGGCTCTT 340	Qy 41 LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg 60 Dh 341 CTTCCAGARAAGACAAGACAAGAGAAGACAACAATGACAAAGACAATGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGAAAGACAAGAAAGACAAAGAAAGAAAGAAAAGACAAAGAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAAGAAAA	61 GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrlleGly 		101 ProteuGluSerGluIleIleIleAspAspGlyGlnPheGlyIleHisAsnGlyValGlu	121 ThrieussperdlyTrpLeuThrCysGlnThrGlulleArgLeuArgLeuHisTyrSer	Qy 141 GluLysProProValSerIleThrLysLysLysLeuLysLysSerArgPheArgValLys 160 Db 641 GAAAAACTCCCTGTGTCCAATAACCAAGAAAAATTAAAAAATTTAGATTTAGGGTGAAG 700	161 LeuthrieugluglyLeugludspaspaspaspasgalserProThrValLeuHis 	Oy 181 LysMetSerAsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCysArgHis 200		Oy 221 ThrMetGluProAspAsnLeuGluLeullePheAspPhePheGluGluAspLeuSerGlu 240	Qy 241 HisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlacysLeuLeuSerSer 260	261 ThrileAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProlleMetSerArgAsn		rcccgaaaacaataggcaaagtgaggttgactatataattattaagccattaccagga	Qy 301 TyrSerCysAspMetLysSerSerPheSerLysTyrLybLysProArg1leProLeuAsp 320	321		-	Qy 361 ValHisLeuSerLySAspPheValProValValTyrHisAspLeuThrCysCysLeuThr 380
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Nagase, T., Kikuno, R., Ishikawa, K.I., Hirosawa, M. and Ohara, O. Prediction of the coding sequences of unidentified human genes. XVI. The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro
DNA Res. 7 (1), 65-73 (2000)
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Ohara,O., Nagase,T. and Kikuno,R.
Direct Submission
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Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
Eax:+81-438-52-3914)
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linear ROD 06-APR-2003 LK44 mRNA, complete cds. uleuProGluLeuLysSerCys 640 buCysGlyGluserAspIleHis 660 nSerglyLysArgArglleVal 500 |||||||||||||||||||||||| TTCTGGGAAGAGGAGAATAGTG 1704 oGluLeuMetAspLeuArgSer 540 |||||||||||||||||||| TGAACTCATGGACCTCAGATCT 1824 STTTAACATTGAAATAAAATGG 1584 480 Vertebrata; Euteleostomi; thi; Muridae; Murinae; 900 Veteran Ave., Warren 68 (2001) 220

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/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/tiseue_type="brain microvasculature"

108. .2126

/note="enriched at the brain microvasculature; similar to Homo sapiens hypothetical protein in GenBank Accession Number XM 045585"

/codon_start=1

/evidence=not experimental

/product="hypothetical protein Lk44"

/product="hypothetical protein Lk44"

/protein_id="AA084024.1"

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/db_xref="fol:25569151"

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LEGLEEDDDDDDAASPTVLHKWISNSLEISLISDNEFKCHSOPECGYGLOPDRWTEYS

IQTMEPDNLELIFDFPEBLSEHVVQGOVLESCNOYOFRICHEPS

IQTMEPDNLELIFDFPEBLSEHVVQGOVLESCNOYOFRICHEPS

IQTMEPDNLELIFDFPEBLSEHVVQGOVLESCNOYOFRICHEPS

IQTMEPDNLELIFDFPEBLSEHVVQGOVLESCNOYOFRICHEPS

IQTMEPDNLELIFDFPEBLSHVVQGOVLESCNOYOFRICHEPS

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IQTMEDNLELIFDFPEBLSHVVQGOVLESCNOYOFRICHEPS

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                                                                                                                                                                                                                                                                                                                                                                                                       AC144439 39694 bp DNA linear HTG 16-APR-2003 Homo sapiens chromosome 7 clone XXFOS-87042G10, WORKING DRAFT SEQUENCE, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      St. Louis,
                                                                                                                                                                                                                      AGATCTCGGACAACACCCATTGCAATGAGCTTTGCACAGTTTGAAAATATTTTGGGGATA 1781
                                                                                                                                             LysGluLeuGlyValAsnGlyLeuileTyrAspArgileTyrAspTrpMetProGluGln 618
                                                                                                                                                                                                      ProAsnIlePheGlnValGluGlnLeuGluArgLeuLysGlnGluLeuProGluLeuLys 638
                                                                                                                                                                                                                                                             SerCysLeuCysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAsp 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 39694)
Waterston,R.H.
                             GlyLeuValilePheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (16-APR-2003) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: pissmid; 100% chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-primer ET; 0% of reads Assembly program: Phrap, version 0.990319 consensus quality: 39167 bases at least Q40 consensus quality: 39319 bases at least Q30 Consensus quality: 39366 bases at least Q20
                                                                                                                                                                                                                                                                                                                       ------ Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC144439
AC144439.1 GI:29893792
ATHGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: H_AA087042G10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: M13; 0%
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2 (bases 1 to 39694)
Waterston, R.H.
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VERSION
KEYWORDS
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       soon as it is available and the accession number will
                         7028: contig of 7028 bp in length
7128: gap of unknown length
16822: contig of 9694 bp in length
16922: gap of unknown length
39694: contig of 22772 bp in length
                                                                                                                                                                                                                                                                          39694
611
17
35
139
6
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Conservative:
Mismatches:
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2992.50
78.50%
76.38%
84.61%
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AUTHORS TITLE JOURNAL

REFERENCE

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JOURNAL

REFERENCE AUTHORS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (08-OCT-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Apr 13, 2002 this sequence version replaced gi:19774659.
                                                                                                                                                                     Submitted (03-APR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA 6 (bases 1 to 149259)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping project (Eric D. Green, Director). John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://genome.map.nhi.mi.gov/DIR/GIB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu
                                          Direct Submission
Submitted (28-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                 Submitted (13-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 0); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Washington University Genome Sequencing Center Center code: WUGSC
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University, 4444 Forest
8 (bases 1 to 149259)
      (bases 1 to 149259)
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                             Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                 Waterston, R.
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REFERENCE AUTHORS TITLE

JOURNAL

TITLE JOURNAL

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

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1. .149259 /organism="Homo sapiens" /mol_type="genomic DNA" Location/Qualifiers

source

FEATURES

/rpt_family="ERV1" .0353. .12161

repeat_region repeat_region repeat_region

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TITCTICATITIGAIGCAGAIAITIGCACAAIGGITIGGCAAAAGGCAGAACAAAIAICCCA 21482
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Direct Submission
Submitted (13-May-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email S.Wiemann@dkfz-heidelberg.de;
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Catarrhini, Hominidae, Homo.
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                       leLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSerA
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Mammalia; Eutheria; Primates;
1 (bases 1 to 6671)
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                                          German Genome Project.
This close (DKF26510715) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
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                                                                                                                                                                             /organism="Homo sapiens"
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/clone lib="451 (syronym: hloc1). Vector pSport1; host
DH10B; sites NotI + SalI"
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sequenced by GBF (National Research Centre for Biotechnology Lt
Braunschweig/Germany) within the cDNA sequencing consortium of
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Gaps:
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99.65%
84.22%
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Best Local Similarity:
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DNA linear HTG 31-JUL-2004
CH251-549B3, WORKING DRAFT
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Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (31-JUL-2004) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center Center code: WUGSC
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8814: gap of unknown length
35261: contig of 2647 bp in length
35361: gap of unknown length
62200: contig of 26839 bp in length
62300: gap of unknown length
114137: contig of 51837 bp in length
114237: gap of unknown length
158156: contig of 43919 bp in length
158256: gap of unknown length
158256: gap of unknown length
158258: gap of unknown length
158728: gap of unknown length
159728: gap of unknown length
160762: contig of 1372 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer BT; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; veraion 0.990319
Consensus quality: 156619 bases at least Q40
Consensus quality: 157310 bases at least Q30
Consensus quality: 157914 bases at least Q20
                                                                             ON Pan troglodytes chromosome 7 clone CH251-549B3, SEQUENCE, 7 unordered pieces.

N AC150686.1 G1:50872649
HTG. HTGS. PHASE1, HTGS DRAFT, HTGS_ACTIVEFIN.
Pan troglodytes (chimpanzee)
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/note="assembly_name:Contig16
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Unpublished
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/organism="Pan troglodytes"
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3393 GATGCCAACGCATTGATAACGTGGAGAATGCT
                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
11 (baees 1 to 160762)
Wilson, R. K.
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Wilson, R.K.
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3273 TTCCAAGTGGAGCAATTGGAACGCCTGAAGCAGGAATTGCCAGAGCTTAAGAGCTGTTTG
SerCygAspMetLysSerSerPheSerLysTyrTrpLysProArgIleProLeuAspVal
                                                                         GlyHisArgGlyAlaGlyAsnSerThrThrThrAlaGlnLeuAlaLysValGlnGluAsn
                                                                                               2373 GGCCATCGAGGTGCAGAAACTCTACAACAACTGCCCAGCTGGCTAAAGTTCAAGAAAT
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                                     2313 AGTTGTGACATGAAATCTTCATTTTCCAAGTATTGGAAGCCAAGAATACCATTGGATGTT
                                                                                                                                                                                                                            HisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThrMet
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                                           sValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSerTh
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Db 131824 TGCGGCGTCGCGCCTGTAACCCCAGCACTTTGGGAGGCCGAGGAGGAGGTGGATCACCTG 131765	Qy 556 556	Db 131764 AGGTCAGAAGTTCAAGATCAGCTTAGTCAACATGGTGAAACCCAGTCTCTACTAAATATA 131705	Qy 556 556	Db 131704 CAAAAATTAGCCGGGCACCGTGGTGGGCACCTGTAATCCCAGCTACTCGGCAGGCTGAGG 131645	Qy 556 556	Db 131644 CAGGAGAATCGCTTGAATCCGGGAGGGGGGGGGGGTTGCAGTGAGTCGAGATCACGCCATTGT 131585	Qy 556 556	Db 131584 GCTCCGGCCTGGGAAACAAGAGCGAAACTTCGTCTAAAAAAAA	Qy 557Gly-IleAsnValHisThrGluAspLeuLeuArgAsnProSerTyrIleGlnGlu 574	Db 131524 CTACTGGAGATAAATGCACATACTGAAGACTTGCTCAGAAACCCATCCTACATTCAAGAG 131465	Qy 575 AlaLysAlaLysGlyLeuValllePheCysTrpGlyAspAspThrAsnAspProGluAsn 594 Db 131464 GCAAAAGCTAARGGACTAATCATATTCTGCTGGGGGGGGGG	614	Db 131404 AGAGAAATTGAAGGAACTTGGAGTTAATGTCTTTTTTTTT	615 MetProGluGlnProAsnIlePheGlnVal-GluGlnLeuGluArgLeuLysGlnGluLe 6	.⊖ ⊾	131296 GCCAGAGTGTAAGGGCTGTTTGTGTCCCACTGTTAGCCACTTTGTTCCCTCATCTTTGTG 1	Qy 654 sGlyGluSerAspIleHisValAspAlaAsnGlyIleAspAsnValGluAsn 671	236	CQ728047 ION Sequence 139 ON CQ728047		ORGANISM Homo sapiens Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Butheria: Primates: Catarrhin: Hominidae: Homo	CE 1 RS Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W.	TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses	JOURNAL Patent: WO 02068579-A 13981 06-SEP-2002; PE Corporation (NY) (US)	FEATURES Location/Qualifiers source 1.1731	/organism="Homo sapiens" /mol_type="unassigned DNA" /db xref="haxon:6606"	ORIGIN	5.65e-246 Length: 2938.00 Matches:	Percent Similarity: 87.65% Conservative: 0 Best Local Similarity: 87.65% Mismatches: 0 Query Match: 83.06% Indels: 81	

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3174) Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.W., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y. Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Schmutz,J., Myers,R.M., Generation and initial analysis of more than 15,000 full-length	human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932 2 (bases 1 to 3174) Strausberg,R. Direct Submission Submitted (26-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact. MGC help desk	Contacts angworm.rmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Glbbs, R.A. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Lull. at: http://image.llnl.gov Series: IRAK Plate: 54 Row: g Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21312645. Location/Qualifiers 1. 3174 / Organism="Mus musculus" // Organism="Mus musculus" // Organism="Mus musculus" // Organism="Maxon:10090" // Clone="MGC:89711 IMAGE:3357683" // Clone="MGC:8711 IMAGE:3357683" // Clone="MGC:8711 IMAGE:3357683"	/lab_host="DH10B""
REFERENCE AUTHORS		FEATURES	gene
	477 eAspMetAsnLeuPheLeuAspIleIleLeuLySThrValLeuGluAsnSerGlyLysAr	QY 577 aLysGlyLeuValllePheCysTrpGlyAspAspThrAsnAspAspTrcGluAsnArgArgLy 597 Db 1443 TAAGGGACTAGTCATATTCTGCTGGGGTGATGATCCTGAAAACAGAAGGAA 1502 QY 597 sLeuLysGluLeuGlyValAsnGlyLeuIleTyrAspArglleTyrAspTrpMetProGl 617 Db 1503 ATTGAAGGACTTAGGGTCTAATTTATGGATAGGATAATTGATTG	

	33 35 35	358 GluPheAspValHisLeuSerLysAspPheValProValValTyrHisAspLeuThrCys 377	LysGluteuThrPheAspGlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLys 417	1193 ACCAAAGACGGAAACAATCTTTGTATGAGGAGGAAATTTCTTTTCTGAAAATCAGCA 1252 438 PheProSerLeulysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGlu 457 	458 IleLysTrp11eCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPhe 477	498 ArgilevalPheSerSerPheAspAlaAspIleCysThrWetValArgGlnLysGlnAsn 517	538 LeuargSerargThrThrProllealaMetSerPheAlaGluPheGluAsnLeuLeuGly 557	578
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/db xref="LocusID:74182" /db_xref="LocusID:74182" /db_xref="MG1:1921432" /translation="MGNSLEEELSISNBEFKCRHSQPECGYGLQPDRWTEYSIQTMEPD NLELIFDFFEEDLSEHVVQGDVLPGHVGTACLLGSTIAESGRSAGILTLPIMSRNSRK TIGKWRWDFIIKPLECYSCSMQSSPSKYWFRIPLDVGHRGAGNSTTAKLAKVQBN TIASLRNAASHGAFVEFDVHLSKDFVPVVYHDLTCCLTMKRKYEADPVELFEIPPVKE IJFDOLOLLKLSHVTALKTKNEKQSIYEBRNFFSENOPFPELKMYLESLPENVGFNIE IKWICQHRDGVWDGNLSTYFDMNVFLDIILKTVLENSGKRRIVFSSFDADICTMVRQK QNKYPLILELTQGKSDIYPELMDLKRSTTPIAMSFAQFENILGINAHTBDLLANPSVYQ BAKAKGLVIFGWGDDTNDPERREKLKEFGVNGLIXDRIYDMMPEQPNIFQVEQLERLK QELPELKNCLCPTVSHFIPSSFCVEPDIHVDANGIDSVENA"	Alignment Scores: Pred. No.: Score: Score: Score: Bercent Similarity: Ber Local Similarity: Best Local Similarit	MetThrProSerGlnValalaPheGluIleArgGlyThrLeuLeuProGlyGluVal	Db 193 GCANTATCTGGAAGCTGTCATGCCCTGGGAAACTGGAATCCTCAAAATCCTGTGGCTCTT 252 Qy 41 LeuProGluAsnaspThrGJyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg 60 15:	313 GGAGTGTCAGTGAAGTACCGCTACTTCAGAGGCTGCTTTTTAGAA	101 ProLeuGluSerGluIleIleIleAspAspGlyGlnPheGlyIleHisAsnGlyValGlu 12	GluLysProProValSerIleThrLysLysLeuLysLysSerArgPheArgV	413 CTCACACTCGAGGGTCTGGAGGAAGATGATGATGATGATGACGATAAGGTCTCTCCCACT 4 178 ValleuHisLysWetSerAsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLys 1 1 1 1 1 1 1 1 1	Db 533 TGCAGGCACTCACAGCCAGAATGTGGGTATACAGCCCCGATCGTTGGACAGAGTAC 592 Qy 218 SerileGlnThrWetGluProAspAsnLeuGluLeullePheAspPhePheGluGluAsp 237

378 TCTTCATTTCCAAGTATTGGAAGCCAAGAATACCATTGGATGTTGGCCATCGAGGTGCA 437 327 GlyAsnSerThrThrThrThlaGlnLeualaLysValGlnGluAsnThrIleAlaSerLeu 346	TTCTTT TLYBAS		367 PhevalprovalvaltyrHisAspLeuThrCysCysLeuThrMetLysLysLysPheAsp 386	387 AlaAspProvalGluLeuPheGluIleProvalLysGluLeuThrPheAspGlnLeuGln 406 	407 LeuleulysLeuthrHisValThrAlaLeulysSerlysAspArgLysGluSerValVal 426	GINGluGluAsnSerPheSerGluAsnGInProPheProSerLeuLysMetValLeuGlu 4 	r 60	- 80	87 LeulysthrValleuGluAsnSerGlyLysArgArgIleValPheSerSerPheAspAla 50 	neLeuThrGln TTTAACTCAA	527 GlyLysSerGluIleTyrProGluLeuMetaspLeuArgSerargThrThrProIleAla 546 		985		STTAATGGTCTA 12	607 ileTyraspargileTyraspTrpMetProGluGlnProAsnilePheGlnValGluGln 626 	LeugluargLeuLysGlnGluLeuProGluLeuLysSerCysLeuCysProThrValSer 64	1338 TTGGAACGCCTGAAGCAGGAATTGCCAGAGCTTAAGAGCTGTTTGTGTCCCACTGTTAGC 1397 647 ArgpheValProSerSerLeuCysGlyGluSerAspIleHisValAspAlaAsnGlyIle 666	8 CGCTTTGTTCCCTCATCTTTG	667 ASPABIVALGARATA 8/2
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618 GlnProAsnilePheGlnValGluGlnLeuGluArgLeuLysGlnGluLeuProGluLeu 6	user 65	Db 1853 AAGAACTGTTTGTGTCCCACTGTTAGCCACTTCATCCCTTCTTCTTTGTGTGGAGCCT 1912	Oy 658 AspileHisValAspAlaAsnGlyIleAspAsnValGluAsnAla 672 	RESULT 15 AX127525 LOCUS AX127525 AX127525 AX127525 DNA linear PAT 15-MAY-2001 DEFINITION Sequence 1 from Patent WO0131007.	AX127525. AX127525.1 GI:1413423	Homo sapiens Homo sapiens Eukaryota; Me Mammalia; Eut	AUTHORS Chiang, L.W. TITLE Nucleic acid molecules derived from rat brain and programmed cell death models TOWNERS OF THE CONTRACT AT 102-MAY-2001.	Millenniu ce	/mol type="lucasigned DNA" /db_xref="taxon:9606" ORIGIN	4.35e-212 Length: 2552.00 Matches: 100.00% Conservative:	Mismatches Indels: Gaps:	US-10-047-855-3 (1-672) x AX127525 (1-2738)	18 GAGATATCCTTAATAAGCGACAATGAGTTCAAGTGCAGGCATTCACAGCCGGAGTGTGGT	Qy 207 TyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGlnThrMetGluProAspAsn 226	227	erGly	198 GCCTTCCTGCATGTGGGTACAGCTTGTCTTTATCATCACCACTTGCTGGAGA	TAGGC 31	Oy 287 LygValArgValAspTyrIleIleIleLysProLeuProGlyTyrSerCysAspMetLys 306	307

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